Wed Sep 10 10:15:41 2003

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OM protein - protein search, using sw model

Run on:

August 13, 2003, 15:21:20 ; Search time 47.9168 Seconds (without alignments) 2698.100 Million cell updates/sec

US-09-303-232-6 2640 1 MAPMLAALALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 Total number of hits satisfying chosen parameters: 830525 segs, 258052604 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_23:\*
1: sp\_archea:\*
2: sp\_bacteria:\*

sp\_fung1:\*
sp\_human:\*
sp\_lnvertebrate:\*
sp\_mammal:\* sp\_vertebrate:\*
sp\_unclassified:\* sp\_mhc:\* sp\_organelle:\* sp\_phage:\* sp\_rvirus:\* sp\_bacteriap:\* sp\_plant:\* sp\_rodent:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

#### SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
				÷		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1	2640	100.0	501	Ŋ	Q9X2I4	Q9xzi4 heliothis v
7	2194	83.1	494	Ŋ	Q8T7S1	Q8t7s1 drosophila
e	2181	82.6	494	Ŋ	Q8T7S2	08t7s2 drosophila
4	2177	82.5	494	'n	Q8T7S3	08t7s3 drosophila
'n	2176.5		509	Ŋ	Q8T7S0	08t7s0 drosophila
<b>9</b>	2156.5		523	Ŋ	Q8T7R9	08t7r9 drosophila
7	1833		554	S	09VL79	09v179 drosophila
60	1803.5		496	Ŋ	Q9XZI3	Q9xzi3 heliothis v
6	1800.5		807	'n	Q8T7V5	08t7v5 drosophila
10	1786.5		545	Ŋ	61W160	O9vwi9 drosophila
11	1705.5		525	Ŋ	Q8IPE2	Q8ipe2 drosophila
12	1258.5		502	11	9днр6	Ogihd6 mus musculu
13	1226.5	46.5	511	13	003481	003481 gallus gall
14	1145.5		480	S	081932	081932 caenorhabdi
15	1132	42.9	461	Ŋ	P91197	P91197 caenorhabdi
16	1124	42.6	273	Ŋ	Q9VJT9	Q9vjt9 drosophila

42 5 062083 42 5 018556 33 5 08MKD1 15 5 066133 37 5 09U941 04 11 08W44 99 11 08W44 99 11 08W46 99 13 08WR51 10 08WR51 10 08WR51 10 08WR51 10 08WR51 10 08WR51 11 08WW51 11 08WW51 11 08WW61 11 08W61 11 08WW61 11 08WW61 11 08WW61 11 08WW61 11 08WW61 11 08W61 11 08W61 11 08W	554 5345 5345 5454 5	062083 caenorhabdi Q18556 caenorhabdi Q9nkdl drosophila Q8murQ apis mellif O46133 locusta mig	0.40	USYCT A GOSUPHILA O96632 hellothis v O46128 hellothis v Q8COQ9 aplysia cal P91765 myzus persi		O46115 IOOUSTA MIG QBmub6 aphis gossy QBKda7 mus musculu P91764 myzus persi QGPW9 mus musculu	Qospuo Dos Laurus O96633 heliothis v Q91x60 mus musculu Q918c7 gallus gall Q8r493 mus musculu
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## ALIGNMENTS

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			į.	ota;	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoldea;					"Putative alpha subunits of insect nicotinic acetylcholine receptors	more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than	ounit		-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY										or;			01;	0;
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MA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Grauso M., Renana R.A., Culetto E., Sattelle D.B.;
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Tovol Putative Nicotinic Acetylcholine Recep
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
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Ephydroidea; Drosophilidae; Drosophila.
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-:- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
-- SIAP21446; AAM133931. :
-- Flybase; FBgn0032151; nAcR-alpha-30D.
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MEDLINE-21969411; PubMed=11973307;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify

Mediated Alphy Conserved Target of Adenosine Deaminase Acting on R

Mediated A-to-1 Pre-mRAR Editing.",

Genetics 160:1519-1533(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic accetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda: Hexapoda; Insecta: Pterygota;
                                        Length 494;
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Ephydroidea; Drosophilidae; Drosophila,
                                                                                   Indels
                                                                                37;
                                      ; Score 2194; DB 5;
; Pred. No. 5.7e-198;
31; Mismatches 37;
48327537229573FF
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Interpro; IPR006202; Neur_chan_LBD
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                                          83.1%;
82.6%;
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  56113
                                                              al Similarity 82.6
418; Conservative
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494 AA;
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CLEVETLETIIATVAVLLSAPHIIVQ
                                                                                                                                                                    494 AA;
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                                                                                                                                                                    SEQUENCE
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409 ASFGRPTIVEEHHTAIGCNHKDLHLILKELQFITARMRKADDEAELIGDWKFAAMVVDRF 468
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                                                                                                                                                                2 APMLAALAL-----LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLT
                                                                                                                                                                                                                                                                                                                   DLVLKDEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFF
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                                                                                                                                           Gaps
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                                                                                                                                           20;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MNR-2003 (TrEMBLrel. 23, Last annotation update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                               Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                  Length 494;
                                                                                                                                           Indels
                                                                                       494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;
                                                                                                                                           38;
                                                                                                               Score 2181; DB 5;
Pred. No. 9.6e-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                        35; Mismatches
             Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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InterPro; IPR006029; Neu_channel_memb.
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                                                                                                                82.6%;
81.6%;
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                                                                                                                                        Matches 413; Conservative
                                                                                                                            Local Similarity
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                                                                             Transmembrane
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63 LQQIIDVDEKNQILTTNAWLNLEWNDYNLRWNETEYGGVKDLRITPNKLMKPDVLMYNSA 122
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARIY-
-:- SIMILARIY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
EMBL; AF321445; AAM13392.1; -
FLYBRSE; FERO0032151; nAck-alpha-30D.
                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                          Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                          Length 494;
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.5%; Score 2177; DB 5; Best Local Similarity 81.8%; Pred. No. 2.3e-196; Matches 414; Conservative 33; Mismatches 39;
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                                                                                                     Interpro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR00629; Neur_channel_memb
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_LBD; 1.
TIGRPAM; TIGR0060; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
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NCBI_TaxID=7227;
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Ephydroidea; Dr
NCBI_TaxID=7227
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                                                                                                                                                                                                              5; Length 509;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                        Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                          509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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                                                                                                                                                                                                            82.4%; Score 2176.5; DB 5;
80.2%; Pred. No. 2.7e-196;
ive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        523 AA
                                                                                                                                                   TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                     Flybass; F8970032151; nACR-alpha-30D. InterPro; IPR006201; Neur_channel. InterPro; IPR006202; Neur_channel. InterPro; IPR006303; Neur_channel_memb. Pfam; PF02931; Neur_chan_LBD; 1.
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Matches 418;
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2 APMLAALAL -----LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLT
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MEDLINE-21969411; PubMed-11973307;
Grauso M., Renan R.A., Culetto E., Sattelle D.B.;
Grauso M., Reman R.A., Culetto E., Sattelle D.B.;
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-tor. Pre-mRNA Editing.";
Mediated A-tor. Pre-mRNA Editing.";
elentics 160:1519-1533(2021.
elentics 160:1519-1533(2
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Endopterygota; Diptera; Brachycera; Muscomorpha;
ea; Drosophilidae; Drosophila.
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PROSITE; PS00236; NEUROTR_ION_CHANNEL;
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RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Randrides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Randrides R.A., Lewis S.E., Richards S., Ashbunner M. Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Channe M., Pielifer D.,
RA Mr. H., Doyle C. Baxer E.G., Helt G., Channe M., Pielifer D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Bocken M.R., Bouck J., Bayraktaroglu L., Basaley E.M.,
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RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chance C., Gabriellan A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeeyam C.,
J., Harvey D., Heiman T.J., Wei M.-H., Ibeeyam C.,
J., Moult S.M., Moy M., Murphy B., Murphy L., Marsiy D.M., Nelson D.L,
Merkulov G., Milshina N.V., Li J., Li Z., Liang Y., Lin Z.,
Liang Y., Lin X.,
Ralander K., Ranington K.A., Nobarry C., Morbherson D.,
Relson D.R., Nolson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Rollamet K.M., Moy M., Murphy B., Murphy L., Muskern D.K., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Ralazzolo M., Pittman G.S., Pan S., Pollard Y., Puri W., Shen B.C.,
Siden-Klamos I. Simpson M., Subsebach T., Wang S., Yan G., Shen H.,
Spier E., Spradling A.C., Siapleton M., Subsebach S.,
Ralinams S.M., Woodage T., Worlex C., Web., Shong S., Nan
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Celuiker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Change M., Davenport L.B., Dietz S.M.,
Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Refriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
I begwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A Gonzalez M., Moy M., Murphy B., Neison C., Nelson K.A., Nunco J.,
R. Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
R. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Sequencing of Drosophila melanogaster genome.";
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                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                      CG4128 protein.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                  STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
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NCBI_TaxID=7227;
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                                                           S.E.;
                                                                                                                                                             S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 554;
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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FlyBase; FBQn003151; nacR-alpha-30D.
InterPro; IPR006201; Neur_channel.
InterPro; IPR0060201; Neuchannel.memb.
Pfam; PF02932; Neur_chan_memb; 1.
PIGRFAMS; TIGR08609; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
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65.0%; Pred. No. 7.4e-164;
iive 36; Mismatches 67;
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Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 PPPPDLELERERSSKSLLANVLDIDDDFRH----PQAQQ------PQCCRY---YRGG--- 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EENGAGLAAHSCFGVDYELSLILKEIRVITDOMRKDDEDADISRDWKFAAMVVDRL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 STYPTNVVRNNGSCLYVPPGIFKSTCKIDITWPPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                             Schulter T., Oellers N., Adamczewski M.;

Schulter T., Oellers N., Adamczewski M.;

"Putative alpha subunits of insect nicotinic acetylcholine receptors

ore similar to vertebrate alpha? Subunits and C. elegans Ce21 than

to other insect nicotinic acetylcholine receptor alpha subunits.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN (BY SIMILARITY).

1. SUBCELLULAR PROCATION: INTEGRAL MEMBRANE PROFEIN (BY SIMILARITY).

2. ISIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

3. RHS1, AR143846; AAD32697.1;

3. InterPro; IPRO06502; Neur_channel.

3. InterPro; IPRO06502; Neur_channel.

3. InterPro; IPRO06502; Neur_channel.

3. InterPro; IPRO06502; Neur_channel.

3. PROM PERM; PRO05931; Neur_chan_LEBD; 1.

3. PROM; PRO05931; Neur_chan_LEBD; 1.

3. PROM; PRO05931; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 APMLAALALLALLPVSEQ-GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEAGGDLSDFITNGEWYLIGMPCKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRRAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.3%; Score 1803.5; DB 5;
68.7%; Pred. No. 3.8e-161;
iive 53; Mismatches 78;
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Matches 347; Conservative
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLALLPVSEQ----GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----MRELELKERSSKSLLANVLDIDDDFRHG--PPPPNSTASTGNLGPGCSIFRTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-21969411; PubMed-11973307;

MEDLINE-21969411; PubMed-11973307;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-

Mediated A-tc-1 Fre-mRNA Editing.";

Genetics 160:1519-1533(2002).

-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL, AF2727780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro: IPR006029; Neur_chan_LBD.
InterPro: IPR006029; Neu_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
IGRRAMs; ITGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 68.2%; Score 1800.5; DB 5; Length 11 Similarity 66.3%; Pred. No. 1.5e-160; 348; Conservative 61; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C8B4F6B34287C8C8 CRC64;
                                  AA.
                                  807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF272778; AAM13390.1; –.
Flybase; FBgn0028875; nAcR-alpha-34E.
                                                                                                 Created)
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                                                                                             01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
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0877V5
1D 0877V5
DT 01-JUN----
DT 01-JUN----
DT 01-JUN----
DE Nicotin
GN NACK-ALI
GN NACK-
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Adams M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,
Adams M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,
R. Adams M.D. Celniker S.E., Hill R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
R. Burdon R.C., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
R. Brandon R.C., Rogers Y., Helf G., Nelson C.R., Miklos G.L.G.,
R. Abril J.F., Agbayani A., Baxendale J., Bayerktaroglu L., Beasley E.M.,
Ballew R.M., Basu M., Baxendale J., Bayerktaroglu L., Beasley E.M.,
Ballew R.M., Basu M., Baxendale J., Brokstein P., Brottler P.,
Burkis K.C., Busam D.A., Bulter H., Cadleu E., Center A., Chandra I.,
R. Berson K.Y. Bencs P.V., Berman B.P., Brokstein P., Brottler P.,
Burkis K.C., Busam D.A., Bulter H., Cadleu E., Center A., Chandra I.,
R. Berson K.Y., Evengeliste C., Ferraz C., Ferriera S., Fleischman W.,
R. Berson K.J., Evangeliste C., Ferraz C., Ferriera S., Fleischman M.,
R.J. Berson K.J., Bounes B., Galbeil M., Gabielian A.E., Garriellan A.E., Garriellan A.E., Garriellan A.E., Garriellan A.,
Burbin K.J., Evangeliste C., Ferraz C., Ferriera S., Fleischman M.,
R.J. Huston B.E., Moylan B., Mirphy L., Mizris M.,
Jalali M., Kalush F., Kalpen G. H., Ke Z., Guban P., Harris M.,
Jalali M., Kalush F., Kalpen G. H., Ke Z., Guban P., Harris M.
Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum
Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum
Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum
Jalali M., Kalush F., Kalpen G. H., Ke Z., Kennison J.A., Ketchum
Jalali M., Kalush R., Morttsh T., Moyla, Murphy L., Muzny D.M., Nelson D.K.
Jalali M., Kalush R.A., Nixon K., Nuszny D.M., Nelson D.K., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puzi V., Wassaman D.A., Weilsen B.C., Siden Kiamos I., Simpson M., Stupski M., Wang Z.-Y., Wassaman D.A., Weilsen D.C., Shen H.,
Syleras R., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S. E., Adams M. D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Bancon J., An H., Baldwin D., Bancon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
02(3)2538 protein.
NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                        DEEAELISDWKFAAMVVDRFCLFVFTLFTILATVAVLLSAPHILV
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
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                                                                                                                                                                Q9VWI9
                                                                                                                 RESULT 10
                                                                                                                                          09VWI9
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80 NDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVVVRSGGSCLYVP 139 PGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLI 199 466 369 KERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMED-- 426 20 GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQLLITNIWLSLEW 79 39 GPHEKRLLHALLDNYNSLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW 260 EKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHH 320 RTADIHEMPOWIKSVFLOWLPWILRMSRPGK------KITRKTIMMNTRMRELEL -----VGGGL-----GSHHRELHLILRELQFITARMKKADEEAELISDWK Gaps Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zavori J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E.; Smith C.D., Tupy J.L., Berqman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris h Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Indels 45; DB 5; Length 545; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003511; AAF48950.2; -. FlyBase; FBGN0031014; nAcR-alpha-18C. InterPro; IPR006201; Neur\_channel. InterPro; IPR006202; Neur\_channel. InterPro; IPR006202; Neur\_channel\_memb. Pfam; PF02911; Neur\_chan\_LBD; 1.
Pfam; PF02932; Neur\_chan\_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TTGE00860; LIC: 1.
PROSITE; PS00236; NEUROTR\_ION\_CHANNEL; 1.
SEQUENCE 545 AA; 61517 MW; 7B83025107A66209 CRC64; 67.7%; Score 1786.5; DB 5; 66.7%; Pred. No. 1.8e-159; ive 56; Mismatches 70; 343; Conservative Query Match Best Local Similarity SEQUENCE FROM N.A. SECUENCE FROM N.A. SEQUENCE FROM N.A. 140 FlyBase; Matches q ò 8 δλ q g g g qq δ ò ŏ ŏ ò

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RA MEDLINE—20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Strton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Strton G.G., Wortman J.R., Plazel R.G., Champe M., Pfeitfer B.D.,

RA Ballew R.A., Bayani A., Bazel R.G., Champe M., Pfeitfer B.D.,

RA Adril J.E., Agbayani A., Bazel R.G., Champe M., Pfeitfer B.D.,

RA Ballew R.M., Basun A., Bazendale J., Andrews-Péankoch C., Baldwin D.,

RA Ballew R.M., Basun A., Bazendale J., Andrews-Péankoch C., Baldwin D.,

RA Barlis K.G., Eusam D.A., Bulck J., Andrews-Péankoch C., Baldwin D.,

RA Barlis K.C., Busam D.A., Bulck J., Brokstein P., Brottier P.,

RA Burlis K.C., Eusam D.A., Bulch H., Cadieu E., Center A., Chandra I.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Plakovo S.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Plasser R.,

RA Poster C., Gabriellan A.E., Gary N.S., Gelbart W.M., Classer R.,

RA Hostin D., Houston R.A., Howland T.J., Herindez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Herindez J.R., Houck J.,

RA Liasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

RA Liu X., Mattel B., Mourphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Minnel B.E., Kodira C.D., Kraft C., Kratiz S., Kulp D., Lai Z.,

RA Minnel B.E., Kodira C.D., Kraft C., Kratiz S., Mulp D., Lai Z.,

RA Minnel B.E., Kodira C.D., Kraft C., McLeod M.P., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Shen E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Stieret K., Remington K.A., Mishson M., Stupski M.P., Smith T.,

RA Stieret K., Remington K., Sauderet R., Vender S., Wang A., Smith H.O.,

RA Shen E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

RA Shen S., Woodager World W., Welsenbach J.,

RA Shen S., Welse B.C., Staden-Kiamos I. Stupson M., Stupses M., Woodager World W., Welsen B.C., Sid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S. E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Perritera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Petel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  FAAMVVDRFCLFVFTLFTIIATVAVLLSAPHIIV
                        525 AA.
                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLVLKDEAGGDLSDFITNGEWYLIGM-PGKKNTITYACCP------EPYVDVT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 -----ILFFQFNCAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKPCRRVH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 APMLAALAL-----LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 ------TILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 VVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMRELELKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 SKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVL
                                                                                                                       Campbell K.
                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Sarle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 FTIMIRRRTLYYFFNLIVPCVLISSMALL----GFTLPPDSGEKLTLGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 64.6%; Score 1705.5; DB 5; Length Local Similarity 63.2%; Pred. No. 7.3e-152; nes 347; Conservative 43; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE003626; AAN10709.1; - SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                           (MAR-2000) to the EMBL/GenBank/DDBJ databases
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517 LSAPHIIVO 525
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                     SEQUENCE FROM N.A.
                                                                 Submitted
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RESULT 12 Q9JHD6

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"Superfamily."

"Superfamily."

"Superfamily."

"Superfamily."

"Neuron 5:35-48(1990).

"I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

"I SUMLENTRY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

"I SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

"I THEAPTO: IPRO06201; Neur_channel.

"I THEAPTO: IPRO06202; Neur_channel.

"I THEAPTO: IPRO06203; Neur_channel...memb.

"I THEAPTO: IPRO0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 TNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 ASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMR 364
      418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCL
                                        01-MAR-2003 (TrEMELTEI. 23, Last annotation update)
Alphas subunit of nicotinic acetylcholine receptor precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; "Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal subtypes of this branch of the ligand-gated ion channel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 511;
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10F362D153EC87A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                  511 AA.
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                                                                                                                                   FVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                     473 MAFSVFTIICTIGILMSAPNFV 494
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Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
MGD; MGI:99779; Chrna7.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stitzel J.A., Farnham D.A., Collins A.C.;
"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alphabungarotoxin binding in brain.";
Brain Res. Mol. Brain Res. 43:30-40(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 1258.5; DB 11; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.8%; Pred. No. 9.6e-110;
tive 77; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 AA; 56617 MW; C9353E5136D620E3 CRC64;
                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Nicotinic acetylcholine receptor subunit alpha 7.
   502 AA.
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PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
                                                                   Created)
   PRT;
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Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DBA/21bg;
MEDLINE=97189245; PubMed=9037516;
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PRELIMINARY;
                                                                (TrEMBLrel.
                                                                                                                                                                                                                           Mus musculus (Mouse)
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01-OCT-2000 (
01-MAR-2003 (
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Matches
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us-09-303-232-6.rspt

358 359

	Qy 301 MEMVASSVVLTVVVVLNYHRTADIHEMPQWIKSVFLQWLPWILEMSRPGKKITRKTIM 3	QY 359 MNTRWRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCS.4   :	QY 409 IFRTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELIS 4	Oy 464 DWKFAAMV 471 :       Db 462 NWKFAAMV 469	RESULT 15 P91197 DD P91197 AC P91197, PRELIMINARY; PRT; 461 AA. AC P91197; TEMBLEEL 03, Created) DT 01-MAY-1997 (TrEMBLEEL 03, Last sequence update) DT 01-MAR-2003 (TrEMBLEEL: 23, Last annotation update) DE Hypothetical 52.7 kDa protein.	GN D2092.3.  GN Caenorhabditis elegans.  OC Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  OC Rhabditidae; Peloderinae; Caenorhabditis.  OX NCBI_TaxID=6239;  RN [1]  RP SEQUENCE FROM N.A.  RC STRAIN-BEISIGO N.2.  RC MEDI.INE-99069613; PubMed=9851916;			InterPro; IPR006029; Pfam; PF02931; Neur_ PF02931; Neur_ PRNINTS; PR00222; NRIC TIGRFAMS; TIGR00860; PROSITE; PS00236; NEI Hypothetical protein; PSGUENCE 461 AA; 5	
:  :  :   :   :  : :::         :  :	365 ELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIF 410	y 411 RTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITAR 451	y 452 MKRADEBAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499 	SSULT 14 31932 3 081932 PRELIMINARY; PRT; 480 AA.	C Q81932; O1-WAR-2003 (TrEMBLrel. 23, Created) O1-WAR-2003 (TrEMBLrel. 23, Last sequence update) T O1-WAR-2003 (TrEMBLrel. 23, Last annotation update) T Acetylcholine receptor protein 16, isoform b. N ACR-16. S Caenorhabditis elegans. S Eukaryota; Metazoa; Nematoda: Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.	K NCHL_TAXID=6239; 1   1] 2 SEQUENCE FROM N.A. 3 SEQUENCE FROM N.A. 5 STRAIN-Bristol N2; 6 WEDLINE-99069613; PubMed=9851916; 7 Waterston R.; 7 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; 5 Science 282:2012-2018 (1998).	N [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Waterston R.; Submitted (DEC-2002) to the EMBL/GenBank/DDbJ databases. EMBL, AF022973; AAN84815.1; N Receptor. SEQUENCE 480 AA; 55274 MW; B5D6B707E50228A3 CRC64;	Query Match 43.4%; Score 1145.5; DB 5; Length 480; Best Local Similarity 47.3%; Pred. No. 4.1e-99; Matches 231; Conservative 71; Mismatches 135; Indels 51; Gaps 9;  2 APMLALLALLEVSEQGPHEKRLINALLENVITERPVANESEPLEVRFGITLQQIID 61 11   1   1   1   1   1   1   1   1   1		D 180 ATGGFDISEYISNEWALPLTTVERNEKFYDCCPEPYPDVHFYLHMRRTLYGGFNLIMP 239  Y 241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300

Search completed: August 13, 2003, 15:29:11 Job time : 49.9168 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein . protein search, using sw model

August 13, 2003, 15:14:55; Search time 10.4907 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-6 2640 1 MAPMLAALALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:.

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	P36544 homo sapien	P49582 mus musculu	gal	Q05941 rattus norv	_	P48180 caenorhabdi	P32297 homo sapien	P04757 rattus norv	Q07263 bos taurus		-		P23414 schistocerc	P17644 drosophila		-			rattus	P49581 gallus gall	rattus	P12392 rattus norv	~		P04755 drosophila	P12390 rattus norv	homo sa	P09479 gallus gall	P17787 homo sapien	_	8 rattus	P26153 gallus gall	P30926 homo sapien
	. QI	ACH7_HUMAN	ACH7_MOUSE	ACH7_CHICK	ACH7_RAT	ACH7_BOVIN	ACH1_CAEEL	ACH3_HUMAN	ACH3_RAT	ACH3_BOVIN	ACH1_DROME	ACH3_CHICK	ACH1_MANSE	ACH1_SCHGR	ACH2_DROME	ACH6_HUMAN	ACH2_CHICK	ACH2_HUMAN	ACH3_CARAU	ACH2_RAT	ACH6_CHICK	ACH6_RAT	ACHP_RAT	ACH4_DROME	ACHA_BOVIN	ACH3_DROME	ACHN_RAT	ACH4_HUMAN	ACHA_CHICK	ACHN_HUMAN	ACH4_CHICK	ACHA_RAT	ACHP_CHICK	ACHP_HUMAN
	ength DB	502 1	502 1	502 1	502 1	499 1	498 1	503 1	499 1	495 1	567 1	496 1	516 1	557 1	576 1	494 1	528 1	529 1	512 1	511 1	494 1	493 1	495 1	519 1	457 1	521 1	500 1	627 1	456 1	502 1	622 1	457 1		498 1
*	Match Length	47.7	•	47.5	•	47.0	46.9	37.5	37.0	36.8	36.5				35.7				34.8	34.7	34.7	34.6	34.5	34.4	34.3	34.1	34.1	34.0	33.9	33.9	33.8	33.7	33.7	33.6
	Score	1258.5	1255.5	1253	1246.5			989.5			64.	948.5	946.5	944	943	933	924.5	922.5	919.5	917	915.5	914.5	910.5	908.5	906	006	899.5	897.5	968	895	891	890	890	887
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P04756 mus musculu	P02708 homo sapien	P02711 torpedo mar	P09483 rattus norv	P09484 gallus gall	P02710 torpedo cal	P05377 xenopus lae	P22456 xenopus lae	P45963 caenorhabdi	Q98880 brachydanio	
ACHA_MOUSE	ACHA_HUMAN	ACHA_TORMA	ACH4_RAT	ACHN_CHICK	ACHA_TORCA	ACH2_XENLA	ACH1_XENLA	ACH8_CAEEL	ACHA_BRARE	ACHP_CARAU
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457	482	461	630	491	461	457	457	538	456	466
33.6	33.4	33.4	33.4	33.4	33.2	33.2	32.9	32.9	32.7	32.5
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# ALIGNMENTS

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                                                                                                                                                                                                                                                               *Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7).";
                                                                                                                                                                                                                                                                                                                                               MEDINE-21829512: PubMed=11840567;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Pararits R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parekhi R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., Zvelebil M.J.;
"Cluster analysis of an extensive human breast cancer cell line protein expression map database.";
Proteomics 2:212-233(2002)
-:- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                 Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T., Lee J., Tian J., Glordano T.;
Cloning and sequence of the human a7 nicotinic acetylcholine
receptor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETR: MW-54157.68; METHOD=MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                     Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M., Helnemann S.F.;
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60; GO:000589; C:nicotinic acetylcholine-gated receptor-chan.
GO: GO:000589; F:nicotinic acetylcholine-activated cation-se.
GO: GO:000187; P:activation of MAPK; TAS.
GO: GO:0008187; P:small molecule transport; TAS.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE.
SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L25827; -; NOT_ANNOTATED_CDS. Z23141; CAA80672.1; -.
                                                                                                                                                                                                              MEDLINE-94245214; PubMed-8188270;
                                                                                                                                        Drug Dev. Res. 30:252-256(1993).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 118-129 FROM N.A.
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PIR; G02259; G02259.
PIR; 137185; ACHUA7.
GGDGW; HGNC:1960; CHRNA7.
MIM; 118511; -
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                                  SEQUENCE OF 17-502 FROM N.A.
                                                                                                                                                                             SEQUENCE OF 24-502 FROM N.A.
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                                                                                                                                                                                                                                                                                     nicotinic receptor
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460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                  8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 66
                                                                                                                                                                                                                                                                                                                                                                                                                              10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 G------RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 ELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNL------GPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 ASVEMSAVA------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIFRTDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                      ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                  . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 502;
          Pfam; PF02932; Neur_chan_memb; 1.
PRINTS: PR00282; NRIONCHANNEL.
TIGRFAMS: TIGROOGO, LIC; 1.
PROSITE; PS00236; NBCNOTR, ION_CHANNEL; 1.
POSTSYNAPLIC membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 1.4e-103; 75; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                             4ACS -> AWPAP (IN REF. 8).
D94B3A482EAA0E42 CRC64;
                                                                                                                                                                                                                               N-LINKED (GLCNAC. . . ) (PO
N-LINKED (GLCNAC. . . ) (PO
N-LINKED (GLCNAC. . . ) (PO
N - 5 G (IN REF. 1 AND 7).
S -> N (IN REF. 2 AND 6).
C -> S (IN REF. 2 AND 6).
C -> S (IN REF. 2 AND 6).
                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                   POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 1258.5; 48.6%; Pred. No. 1.46
                                                                                                             ALPHA-7 CHAIN.
                                                                                    SIMILARITY
                                                                                                                                                POTENTIAL
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                                                                                                                                                            POTENTIAL
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                                                              Postsynaptic memorane, Transmembrane; Multigene family.
Pfam; PF02931; Neur_chan_LBD; 1.
                                                                                                                                                                                                                                                                                                                                            56449 MW;
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Best Local Similarity 48.65
Matches 250; Conservative
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90
133
11
13
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375
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2255
2255
3317
4469
4490
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364
375
409
502 AA;
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DISULFID
DISULFID
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CONFLICT
SEQUENCE
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CARBOHYD
CONFLICT
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CONFLICT
CONFLICT
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MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306

LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS

187 187 247 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366

307 307 367

ELKERSS----KSLLANVLDIDDDFR-----HGPPPPNSTASTGNLGPGCSIFRTDFRRS

246

127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186

29

10 LALAAALLHVSLQGEFQRRLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN **QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN**  417

366

422

478 FVFTLFTIIATVAVLLSAPHII 499 

367 ASVELSAGAGPPTSNGNLLYI --GFRGLEGMHCAPTPDSGVVCGRL--ACSPTHDEHLMH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BÝ SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                          acetylcholine receptor.";
Genomics 26:399-402(1995)
-i- PUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN COMPORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                  SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 502;
                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-95324936; PubMed-7601470;
Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;
"Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C9312E5226D120E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 1255.5; DB 1;
49.6%; Pred. No. 2.5e-103;
tive 78; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
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  205
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MGD; WG1:99779; Chrna7.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD;
Pfam; PF02931; Neur_chan_LBD;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
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56631 MW;
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Matches 249; Conservative
  STANDARD;
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490
164
213
                                                                                                    musculus (Mouse)
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90
133
502 AA;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
231
262
296
296
318
470
150
                                                                                   CHRNA7 OR ACRA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                     MEMBRANE.
ACH7_MOUSE
P49582;
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CARBOHYD
SEQUENCE
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                                                                                                    Mus
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TISSUE=Brain;
MEDLINE=91097796; PubMed=1702646;
Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.;
"A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally regulated and forms a homo-oligomeric channel blocked Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; 01-Aug-1991 (Rel. 19, Created)
1-Aug-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor. and MAbs reveal Lindstroem J.; SEQUENCE OF 1-18 FROM N.A. STRAIN-White Leghorn; ITSSUE-Erythrocyte; STRAIN-White Leghorn; PubMed-1425587; MEDLINE-93049204; PubMed-1425587; Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M., Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J. "Brain alpha-bungarotoxin binding protein cDNAs and MADs reve subtypes of this branch of the ligand-gated ion channel gene superfamily."; 502 AA. PRT; MEDLINE=90315158; PubMed=2369519; STANDARD; by alpha-BTX."; Neuron 5:847-856(1990). Neuron 5:35-48(1990). SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=9031; TISSUE-Brain; Matter J.M.; ACH7\_CHICK P22770; 

99

Gaps

27;

Indels

Matches

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Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor. promoter develops during morphogenesis of the central nervous
                                                                                                                                                      Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                       MEDLINE-92049732; PubMed-1719423; Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; P.: "Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- DEVELOPMENTAL STRAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
MEDLINE=93024917; PubMed=1383829;
Galzi J.-L., Devillers Thiery A., Hussy N., Bertrand S.,
Changeux J.-P., Bertrand D.;
"Mutations in the channel domain of a neuronal nicotinic receptor
convert ion selectivity from cationic to anionic.";
Nature 359:500-505(1992).

-I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAY AFFECTS ALL SUBJUITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                 homologous proteins.";
Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Multigene family; 3D\text{-structure}. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                  TISSUE-Brain;
MEDLINE-85270494; PubMed-3860855;
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PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGRO0860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52295; CAA36543.1; -.
EMBL; X68246; CAA48317.1; -.
EMBL; X6856; CAA48576.1; -.
PIR; JN0113; JN0113.
PDB; IKC4; 17-ARR-02.
PDB; IKL8; 17-ARR-02.
                                                        EMBO J. 11:4529-4538(1992)
                                                                                                                                                                                                                                                                                                                                                                        nicotinic receptor.";
Nature 353:846-849(1991).
                                                                                                                                                                                                                                                       [5]
MUTAGENESIS OF LEU-270.
                                                                                                SEQUENCE OF 24-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE.
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DOMAIN
                                          system.
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242 VLISALALLVFLLPADSGEKISLGITVLLSLTVFWLLVAEIMPATSDSVPLIAQIFASTM 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 RRCSLSSMEMNTVSGQQCSNGNMLYI -- GFRGLDGVHCTPTTDSGVICGRM--TCS---- 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 VDEKNQVLTTINIWLQMYWTDHYLQMNVSEYPGVKNVRFPDGLIWKPDILLYNSADERFDA 124
                                                                                                                                                                                                                                                                                                                                                                                                                      125 TEHTNYLVNSSGHCQYLPPGIFKSSCYIDVRMFPFDVQKCNLKFGSWTYGGWSLDLQMQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIM 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 DFRRSFVRPSTMEDVGGGLGSHH-----RELHLILRELQFITARMKKADEEAELISDWKF 467
                                                                                                                                                                                                                                                                                                                                   62 VDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG 121
                                                                                                                                                                                                                                                                                                                                                                                                   122 TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD 181
                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ADISGYISNGEWDLVGIPGKRTESFYECKEPYPDITFTVTMRRRTLYYGLNLLIPC
                                                                                                                                                                                                                                                                   2 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIID
                                                                                                                                                                                                                                                                                   182 EAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 FMVASSVVLTVVVLNYHHRTADIHEMPOMIKSVFLOWLPWILRMSRPGKKITRKTIMMNT
                                                                                                                                                                                                                                    Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                              (BY SIMILARITY).

N-LINED (GLCNAC. .) (POTENTIAL).

N-LINED (GLCNAC. .) (POTENTIAL).

L->S, T: SUPPRESSES INHIBITION BY THE OPEN-TANNEL BLOCKER QX-222.

QR -> ET (IN REF. 3).

QR -> ET (ST325D4309ADZFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE-93147931; PubMed=7678857;
Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
"Molecular cloning, functional properties, and distribution of rat brain alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                47.5%; Score 1253; DB 1; Length 502; 48.8%; Pred. No. 4.2e-103; Live 81; Mismatches 145; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 AAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 AA
                                                                                                                                                                    56946 MW;
                                                                                                                                                                                                                   Best Local Similarity 48.8
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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490
164
213
                                                                 46
90
133
270
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502 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
 TRANSMEM
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
                                  DISULFID
                                                                   CARBOHYD
                                                                                    CARBOHYD
                                                                                                    CARBOHYD
                                                                                                                                                   CONFLICT
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                     Query Match
                                                                                                                   MUTAGEN
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IsoId=P54131-1; Sequence=Displayed;
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473 MAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Adrenal medulla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                      ACH7_BOVIN
P54131;
             127
                                                                               187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAL-LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                         mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
FUNGTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPPRING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                      SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                 SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Transmembrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Mismatches 149; Indels
                                                                  Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA-7 CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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P -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.2%; Score 1246.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                       EMBL; L31619; AAC33136.1; -...
PTR; T01378; T01378.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PP02931; Neur_chan_LBD.
Pfam; PP02931; Neur_chan_LBD. 1.
Pfam; PP02932; Neur_chan_memb; 1.
PrinTS; PR00252; NRIONCHANNEL.
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                                                                                                    STRAIN-Sprague-Dawley; TISSUE-Brain;
                                              STRAIN=Sprague-Dawley; TISSUE=Brain;
          Neurosci. 13:596-604(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56410 MW;
                                                                                                                                                                                                                                                                                                                                             EMBL; S53987; AAB25224.2; -. EMBL; L31619; AAC33136.1; -.
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490
164
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90
133
447
469
502 AA;
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                                  SEQUENCE FROM N.A.
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231
262
296
318
470
150
                                                                                         REVISION TO 363
                                                                                                               Hartley M.;
Submitted (
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 calcium.";
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DISULFID
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CONFLICT
SEQUENCE
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                                                         Boulter
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246 366 GAHPSDGDP------DLAKILEEVRYIANRRCQDESEVICSEWKFAACVVDPLCL 472 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 366 417 367 ASVELSAGAGPPTSNGNLLYI--GFRGLEGMHCAPTPDSGVVCGRL--ACSPTHDEHLMH 422 418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCL 477 BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT FORMS OF THE RECEPTOR. LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 367 ELKERSS----KSLLANVLDIDDDFR-----HGPPPPNSTASTGNLGPGCSIFRTDFRRS "Alpha Bungarotoxin-sensitive nicotinic receptors on bovine chromaffin cells: molecular cloning, functional expression and allernative splicing of the alpha 7 subunit.";

Eur. J. Neurosci. 7:647-655(1995).

-!- FUNCTION. AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; 28-FEB-2003 (Rel. 41, Last annotation update) Neuronal acetylcholine receptor protein, alpha-7 chain precursor. ISOId=P54131-2; Sequence=VSP\_000075; TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS. SIMILARITY: BELONGS TO THE LIGAND-GATED TONIC CHANNEL FAMILY. MEDLINE-95346009; Pubmed-7620615; Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W. Gutierrez L., Criado M.; SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT) 499 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKERSS----KSLLANVLDIDD---DFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFV 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPSEGDP-----DLAKILEEVRYIAHRFRCQDESEAVCSEWKFAACVVDRLCLMA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALLGFTLPPDSGEKLTLGVT1LLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVVVTVIVLQYHHHDPDGGKMPKWTRVVLLNWCAWFLRWKRPGEDKVRPACQHNERRCSL
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                                                                                                                                                                                                                                                                                                                                              NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

Missing (in isoform short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 499;
                                                                                                                                                   InterPro; PPR006029; Neur_channel_memb.
InterPro; IPR006029; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR00521; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00525; NEUROTR_LION_CHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
47.0%; Score 1240.5; DB 1; Length
Best Local Similarity 49.4%; Pred. No. 5.3e-102;
Matches 247; Conservative 78; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                              ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                         EMBL; X93604; CAA63802.1; -.
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161
210
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                               Ballivet M., Alliod C., Bertrand S., Bertrand D.; "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                       28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                  498 AA
                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006020; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
MEDLINE=96196478; PubMed=8627624;
480 FTLFTIIATVAVLLSAPHII 499
                472 FSVFTILCTIGILMSAPNFV 491
                                                                                                                                                                                                                                                                                                                                                          Mol. Biol. 258:261-269(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X83887; CAA58764.1; -. EMBL; AF022973; AAC25796.1; PIR; S68588. HSSP; P58154; 119B.
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493
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212
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                                                                                                                   TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD 181
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                                                           CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI
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                                                  2 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIID
                                                                                                                                                     EAGG-DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRLLYYFFNLIVP
                                                                                                                                                                                                                                                         359 MNTRMRELELKERSSKSLLANVLD-----IDDDFRHGPPPPNSTASTGNLGPGCS
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                     ACH3.HUMAN STANDARD;
PR12297, 015823.2 0956813; 095683; 095683; 096893;
01-0CT-1997 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR NACHRA3.
                                 51;
                Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90245296; Pubmed-2336208;
Fornasari D., Chini B., Tarroni P., Clementi F.;
"Molecular, cloning of human neuronal nicotinic receptor alpha
                                  Indels
E463ABB40AC9FA82 CRC64;
                                                                                                                                                                                                                                                                                                                           DWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                    140;
               Score 1237.5; DB 1
Pred. No. 9.7e-102;
                                80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mihovilovic M., Roses A.D.;
"Expression of mRNAs in human thymus of a neuronal acetylcholine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a neuronal acetylcholine receptor
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurosci. Lett. 111:351-356(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91114756; PubMed=1989896;
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SEQUENCE FROM N.A. (ISOFORM 2)
57169 MW;
                46.98;
                                245; Conservative
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                        Similarity
498 AA;
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SEQUENCE
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Anderson R.E., Jordan H., Moore T., Mang J., Hsheh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A. Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Richards B. W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;
Beneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. (ISOFORM 1).
MEDLINE-97162233; PubMed-9009220;
Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAchR) subunits beta3 and beta4 and expression of seven nachR subunits in the human neuroblastoma cell line SH-SYSY and/OF IMR-32.";
FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNA3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT LEU-21. INS.
MEDI-NE-21342809; Pubmed-11450844;
Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
"Characterization of the human beta4 nAChR gene and polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
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Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez-Norlega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; "Comparative structure of human neuronal alpha 2-alpha 7 and beta expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arredondo J., Grando S.A.; "Cloning cholinergic receptors in human keratinocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TO SUBUNITS: ALPHA AND NON-ALPHA (BETA).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                        J. Mol. Neurosci. 7:217-228(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-99118870; PubMed-9921897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum. Genet. 46:362-366(2001).
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Gaps

61;

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61 DVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                                                  121 GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK 180
                                                                                                                                                                                                                                   181 DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP · 240
                                                                                                                                                                                                                                                                                  241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                                                                                                                                                                                                                                                                                              301 MEMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
                                                                                                                                                                                                                                                                                                                                                                                                         -----TSNEGNAQKPRPLYGAELSNLNCFSRAESKGCKEGYPC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 QDGMCGYCHHRRIKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKA 455
                                                                                                                                                                                                                                                                                                                                                                                  361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL-----GPGCS---- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IFRIDFRRSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKK 454
                                                                                  1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII 60
                                                                                                SEQUENCE FROM N.A.
MEDLINE-88041184; PubMed-2444984;
Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F., Patrick J.;
Functional expression of two neuronal nicotinic acetylcholine receptors from CDNA clones identifies a gene family.";
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor alpha-subunit."; Nature 319:368-374(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR ACRA3.
Rattus norvegicus (Rat).
                                    DB 1; Length 503;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-86118671; PubMed-3753746;
Boulter J., Evans K., Goldman D.J., Martin G., Treco D. Heinemann S.F.,
L -> V (IN REF. 1).
8A9EBC5D71AEC7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 ADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 989.5; DB 1;
; Pred. No. 9.2e-80;
92; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 AA
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          57309 MW;
                                    37.5%;
38.5%;
                                                           Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                 Similarity
           503 AA;
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CONFLICT
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P04757;
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                                    Query Match
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                          IsoId=P32297-2; Sequence=VSP_000073;
Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSLPLALSP -> ALAAPGAVA (IN REF. 2).
LSPP -> CRA (IN REF. 1).
D -> G (IN REF. 1).
DD -> TT (IN REF. 1).
I -> S (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
MALAV -> MGSGPL (in isoform 2).
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EXTRACELLULAR (POTENTIAL)
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            Event=Alternative splicing; Named isoforms=2;
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                                    IsoId-P32297-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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EMBL, U62432, AAB40110.11. -
EMBL, V08418, CAA6595.11. -
EMBL, AJ007783, CAA07682.11. -
EMBL, AJ007784, CAA07682.11. JOINED.
EMBL, AJ007785, CAA07682.11. JOINED.
EMBL, AJ007785, CAA07682.11. JOINED.
EMBL, AJ007787, CAA07682.11. JOINED.
EMBL, BC001642; AAH01642.11. JOINED.
                                                                                                                                                                                                                                                                                                                                   EMBL; BC002996; AAH02996.1; -. EMBL; BC000513; AAH00513.1; -.
                                                                                                                                                                                                                                                                                                                                                           EMBL; AF385584; AAK68110.1; -.
                                                                                                                                                                                                           EMBL; M86383; AAC84176.1; -.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53559; CAA37625.1;
                                                                                                                                                                                                                                                                                                                                                                                             PIR; A53956; A53956.
Genew; HGNC:1957; CHRNA3.
 ALTERNATIVE PRODUCTS:
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289
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PIR; A53956; A53956.
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                         Name=1
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183 AGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCV
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                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                             InterPro; IPR006201; Neur_channel
                                                                                                                                                                                                                                                              474 RFCLFVFTLFTIIATVAVLL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-92319195; PubMed-1620271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X57032; CAA40348.1.; -.
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALEHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 YQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 DEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN.
EXTRACELLULAR.
                                                                                     "Characterization of an acetylcholine receptor alpha 3 gene promoter and its activation by the POU domain factor SCIP/Tst-1."; and its activation by the POU 4094).

J. Biol. Chem. 269:10252-10264(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                           EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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N-LINKED (GLCNAC. .) (PROBABLE).
D66C491E832B9C34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Mismatches 177; Indels
                                                 MEDLINE-94193711; PubMed-8144606;
Yang X., McDonough J., Fyodorov D., Morris M., Wang F.,
Deneris E.S.;
Sci. U.S.A. 84:7763-7767(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                le-78;
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EMBL; U04961; AAA18001.1; -...
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PP02931; Neur_chan_LBD.
Pfam; PP02931; Neur_chan_LBD. 1.
Pram; PR02932; Neur_chan_memb; 1.
Pram; PR02932; Neur_chan_memb; 1.
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40.2%;
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                       SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 201; Conservative
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Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 RSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVD 473
                                                                                                                                                 LISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMF
                                                                                                                                                                                                                                                                  303 MVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRP--GKKITRKT-IMM
                                                                                                                                                                                                                                                                                                                                           308 FVTLSIVITVFVLNVHYRTPTTHTMPTWVKAVFLNLLPRVMFMTRPTSGEGDTPKTRTFY
                                                                                                                                                                                                                                                                                                                                                                                                                        360 NTRMRELELKERS-SKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFR---TDFR
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"Primary Structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";
Neurochem. Res. 17:281-287(1992)
-!- FONCTION: AFFERS BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
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-!- SUBGELLULAR LOCATION: INTEGRAI membrane protein.
-!- SUBGELLULAR LOCATION: INTEGRAI membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S60589; S60589.
InterPro; IPR006029; Neu_channel_memb
InterPro; IPR006202; Neur_chan_LBD.
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7;
                                                                                                                                                                                                                                                                                                                                                                 418
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                                                                                                                                                                                                                                          KNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQ 124
                                                                                                                                                                                                                                                                               125 TNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG 184
                                                                                                                                                                                                                                                                                        244
                                                                                                                                                                                                                                                                                                                                                      SSMALLGFTLPPDSGEXLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMV 304
                                                                                                                                                                                                                                                                                                                                                                                          305 ASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGK---KITRKTIMMNT 361
                                                                                                                                                                                                                                                                                                                                                                                                      366 ELSNLNCFSRIESKVC------KEGYP-----CQDGLCG-YCHHRRAKISNFSANL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 TRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVIDRIF 469
                                                                                                                                                                                                       64
                                                                                                                                                                                                                         99
                                                                                                                                                                                                      LAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE
                                                                                                                                                                                                                        7 LRRLLLLLLLLPVASTSDAEHRLFERLFEDYNEIIRPVANVSDPVIIQFEVSMSQLVKVDE
                                                                                                                                                                                                                                                    GDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI
                                                                                                                                                                                                                                                                                                                               RMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFR---TDFRRSF
membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                       Gaps
                          NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                   BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACHI_DROME STANDARD; PRT; 567 AA.
P09478; 09VC74;
01-MAR-1989 (Rel. 10, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
Bursophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                  DB 1; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                     Indels
                                                                               CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                322825629821EA07 CRC64;
                                   ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
POTENTIAL.
                                                                                                                                                                           ; Pred. No. 4.3e-78; 93; Mismatches 181;
                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                   Score 970.5;
                                                                                           POTENTIAL.
                   POTENTIAL.
                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|| | |: | : |
470 LWVFILVCILGTAGLFL 486
  Transmembrane; Multigene family SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFVFTLFTIIATVAVLL 493
                                                                                                                                                  56914 MW;
                                                                                                                                                                  36.8%;
                                                                                                                                                                  Query Match
Best Local Similarity 39.8%;
Matches 198; Conservative
 Postsynaptic
                                                                                467
487
163
214
                                                                                                                             45
162
495 AA;
                                            22
231
263
296
 Receptor;
                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                   DISULFID
                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                    185
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                                                                                                                               CARBOHYD
                                                                                                                                                 SEQUENCE
                                                       FRANSMEM
                                                                          TRANSMEM
                                                                                            TRANSMEM
                                                                 FRANSMEM
                                             DOMAIN
                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH1_DROME
                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Basu M. Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Barendale J., Bayraktaroly L., Beasley E.M.,
Beacon K.Y., Basu A., Baxendale J., Bayraktaroly L. Bolshakov S.,
RA Burls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chang Burls R.C., Busam D.A., Dahlke C., Daveport L.B., Davies P.,
RA Burls K.C., Busam D.A., Dahlke C., Daveport L.B., Davies P.,
RA Burls K.C., Busam D.A., Dahlke C., Perraz C., Ferriar C., Pertson C.R., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burls K.L., Canjelian A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gunn P., Harris M.
R. Hostin D., Hauvey D., Helman T.J., Hernandez J.R., Herris M.
Alali M., Kalush F., Karpen G.H., Ke Z., Kemiston J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kemiston J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kemiston J.A., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Purl V., Resee M.G.,
RA, Burls M.D., Purl M., Murphy B., Murphy L., Murshy D., Purl V., Reader F., Sahth H..,
RA, Shue B.C., Siden K.A., Nixon K., Potler E., Wang A.H., Wang X.,
RA, Shue B.C., Siden K.A., Nixon K., Sulpeki M., Sulpe D.C., Shenet F., Santh H.,
RA, Wang Z.-Y., Wassarman D.A., Wenter E., Wang G., Zhu X., Smith H.O.,
RA, Zhong F. W., Woodage T., Wenter E., Wang G., Zhu X., Smith H.O.,
RA, Cheng X.H., Zhong F.N., Woly W., While Sceneber F., Shu H.,
Sylier E., Spradling A.C., Stapheton W., Stung S.,
RA, Shue B.C., Stapheton W., Shue B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: CNS IN EMBRYOS.
DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Stapleton N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN COMPOMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                             from
                                                                             OSSY B., Ballivet M., Spierer P.;
Conservation of neural nicotinic acetylcholine receptors
                                                                                                                                                               Drosophila to vertebrate central nervous systems. EMBO J. 7:611-618(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006; PubMed-10731132;
STRAIN=Oregon-R;
MEDLINE=88283626; PubMed=2840281;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARVAE STAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                           Bossy
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                           SEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAP 496
                                                                                                                       CFESVEEDWKYVAMVLDRMFLWIFAIACVVGTALIILQAP 535
VLGPGC----SIFRTDFRRSFVRPSTMEDVGGGLGSHHR 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JETYLCHOLINE, THE ACHR RESPONDS BY AN AMATION THAT AFFECTS ALL SUBUNITS AND A-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                egral membrane protein.
LEVELS IN THE DEVELOPING CILIARY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                quence update)
notation update)
or protein, alpha-3 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMS TO BE COMPOSED OF TWO DIFFERENT ND NON-ALPHA (ALSO CALLED BETA). A TO CONSIST OF TWO ALPHA-CHAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        777;
ra S., Rungger D., Bertrand S.,
rand D.;
pha 3. Three clustered avian genes
oetylcholine receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226;
Couturier S., Ballivet M.;
define three distinct neuronal
cors.";
                                                                                                                                                                                                                                                                                                                                                          496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006029; New_channel_memb.
InterPro; IPR006202; Newr_chan_LBD.
InterPro; IPR006201; Newr_channel.
Pfam; PF02931; Newr_chan_LBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1990).
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             西
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                                                                                                                                                                                                                                                                                                                                                                                                                              123 YQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 AGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-MNLKDYWESGEWALIKAPGYKHDIKYNCCEBIYTDITYSLYIRRLPLFYTINMIIPCL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 MVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 PGCSIFR-----TDFRRSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKKAD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 MACSCCQYQRMKFSDFSGNLTRSSSSESVDPLFSFSVLSPEMRDAIESVKYIAENMKMON 450
                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                          7 ALALLALLPVSEQG----PHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDV 62
                                                                                                                                                                                                                                                                                                                                                                                     6 ALLLTAAVCILFQGGGGSEPEHRLYAALFKNYNQFVRPVKNASDPVIIQFEVSMSQLVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMF
                                                                                               ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARAL).
                                                                                                                                                                                                          BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                           (bf SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                    Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 FVTLSIVITVEVLNVHYRTPKTHTMPVWVRTIFLNLLPRIMFMTRP----
                                                        Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 MRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLG----
                                                                                                                                                                                                                                                                           FD25BC02A9B601FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLL 493
                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                  Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: |||: |||: || |: |
EAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFL
                                                                                                                                                                                                                                                                                                   Score 948.5; DB 3
Pred. No. 3.8e-76
                                                                                               NEURONAL ACETYI
ALPHA-3 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 AA
                                                                                                                                                                                 CYTOPLASMIC.
                                           PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                 89;
                                                                                                                                                                                                                                                                            57027 MW;
                                                                                                                                                                                                                                                                                                       35.9%;
37.7%;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                   46
                                                                                                 496
                                                                                                                                                                                                                                                                163
496 AA;
                                                                                                                                                                                                                                                                                                                 Local Similarity
es 195; Conserv
                                                                                                                           233
232
264
2298
320
4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH1_MANSE
P91766;
                                                                                                                                        TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                DOMAIN
TRANSMEM
DISULFID
DISULFID
                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                           DOMAIN
                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12.
ACH1_MANSE.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 NGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISSMALLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00236; NEUROFR_ION_CHANNEL; 1. Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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                                                                                                  MEDLINE-98424077; PubMed-9753155; Easthake J.L., Clarke B.S., Towner P., Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P., Reynolds S.E., Wolstenholme A.J., Wonnacott S.; Characterization of a nicotinic acetylcholine receptor from the insect Manduca sexta."; Eur. J. Neurosci. 10:879-889(1998).

Eur. J. Neurosci. 10:879-889(1998).

Eur. J. NEUROSCI. 10:879-889(1998).

EL J. FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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N-LINKED (GLCNAC. .) (POTENTIAL).
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRICHANNEL.
IIGRFAMS; TIGR00860; LIC; 1.
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516 AA;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Gutton G.G., Scherer S.E., I.I. P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Baytaktarolu, Bolshakov S.,
RA Besson K.Y. Bencos P.V., Berman B.P., Bhandari D., Botchier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Changer S.,
Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferraz C., Ferraz C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Bratis N.L., Harvey D., Helman T.J., Hernandez J.R., Harvey B.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
A dalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Malush R.N., Moharry C., Morier J., Wobhrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Bazazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Preese M.G.,
RA Shue B.C., Siden-Kiamos I. Simpson M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Shirkas R., Webrer E., Wan G., Shen H., Web R.,
RA Shirkas R., Webrer E., Web G., Shen H.,
RA Shirkas R., Webrer C., Turner R., Venter E., Wen G., Shen L.,
RA Shirkas R., Webrer G., Shen H., Shong S., Zho O., Sheng L.,
RA Shirkas R., Weber C., Shen H., Shong S., Zhon S., Zhon S., Zhon S., Zhon S., Zhon S., Zhon S.,
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"Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
a novel developmentally regulated alpha-subunit.";
EMBO J. 9:2671-2677(1990).
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
                                                                                                                                       Baumann A., Jonas P., Gundelfinger E.D.; "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila nicotinic acetylcholine receptors"; Nucleic Acids Res. 18:3640-3640(1990).
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDIG ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-TISSUE SPECIFICITY: CNS IN EMBRYOS.
DEVELOPMENTAL STAGE: LATE EMBRYONIC AND LATE PUPAL STAGES.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY. ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY). N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL). Length 576; 35.7%; Score 943; DB 1; Length 576 36.9%; Pred. No. 1.4e-75; tive 102; Mismatches 189; Indels EXTRACELLULAR (POTENTIAL) N-LINKED (GLCNAC. . .) (P 97D6A46CADC3F42F CRC64; CYTOPLASMIC (POTENTIAL) SUBCELLULAR LOCATION: Integral membrane protein. POTENTIAL. BY SIMILARITY LIKE CHAIN POTENTIAL. POTENTIAL. POTENTIAL. Interpro; IPR006029; Neu\_channel\_memb Interpro; IPR006202; Neur\_chan\_LBD. Interpro; IPR006201; Neur\_channel. PROBABLE FlyBase; FBgn0000039; nAcR-alpha-96Ab Pfam; PF02931; Neur\_chan\_LBD; 1. Pfam; PF02932; Neur\_chan\_memb; 1. PRINTS; PR00252; NRIONCHANNEL. ransmembrane; Multigene family Conservative 102; EMBL, X53583; CAA37652.1; -EMBL, AE003748; AAF55303.1; -EMBL, AX058446; AAF13675.1; -PIR; S11679; ACFFA2. 65506 MW; EMBL; X52274; CAA36517.1; -. 65 254 FIGRFAMS; TIGRO0860; 65 254 2 570 5 197; Conserv 85 TRANSMEM TRANSMEM Query Match RANSMEM TRANSMEM DISULFID DISULFID CARBOHYD CARBOHYD CARBOHYD SEQUENCE Best Local Matches 19 SIGNAL DOMAIN DOMAIN CHAIN g q q δy ò δ

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A Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., MoEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                             | : :|||| : :||| : VTTATNRF--SGLVGALGGGLSTLSGYNGLPSVLSGLDDSLSDVAARKKYPFELEKAIHN
                                                                        GTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKIT
                                                                                                         354 RKTIMMNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNS-TASTGNLGP-GCS-IF
         FFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLL
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                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                ACHG_HUMAN STANDARD; PRT; 494 AA.
015825;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebihara M., Ohba H., Yoshikawa T.;
Alu and other elements in the promoter of human nAChR A6
(CHNRA6) direct transcriptional repression.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                          411 RIDFRRSFVRPSTMEDVGGGLGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Substantia nigra;
MEDLINE-97062879; PubMed-8906617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-6 CHAIN, EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606888; .. Goodinic acetylcholine-gated receptor-chan. ..; 60: 00:0005892; C:nicotinic acetylcholine-activated cation-se. ..; 60: 00:0004889; F:signal transduction; TAS. 60: 00:0006832; P:signal transduction; TAS. 60: 00:0006832; P:small molecule transport; TAS. 60: 00:0006832; P:synaptic transmission; TAS.
                                                                                                                                        human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: AFTER BINDING ACCTYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                       IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1A437E6DEE02ABFE CRC64;
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                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
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40.2%; Pred. No. 9e-75;
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; Neur_chan_memb; 1.
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EMEL; AB079246; BAC06855.1; --
EMBL; AB079247; BAC06855.1; JOINED.
EMBL; AB079249; BAC06855.1; JOINED.
EMBL; AB079249; BAC06855.1; JOINED.
EMBL; AB079250; BAC06855.1; JOINED.
EMBL; BC014456; AAH14456.1;
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SEQUENCE
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Matches
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:     ::   : KLRWDPMEYDGIETLRVPA	FKSTCKMDIAWFPFDDQHC    :      :      :	FKSSCPMDITFFPFDHQNC	MPGKKNTITYACCPEPYVD	ASGYKHDIKYNCCEEIYTD	KLTLGVTILLSLTVFLNLV	KVTLCISVLLSLTVFLLVI	TADIHEMPQWIKSVFLQWI	TPTTHTMPRWVKTVFLKLI	LDIDDDFRHGPP	HGEPRHLKECF	GGLGSHHRELHLILRELQF	SEHSPEVEDVINSVQF	489 VAVLL 493	480 AGLFL 484
94		154	201	211	261	271	321	331	381	386	429	423	489	480
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Search completed: August 13, 2003, 15:26:13 Job time: 12.4907 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

August 13, 2003, 15:21:45; Search time 18.7131 Seconds (without alignments) 2574.698 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-303-232-6 2640 1 MAPMLAALALLALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	nicotinic acetylch		nicotinic acetylch	alpha 7 neuronal n	, nicotinic receptor	nicotinic acetylch	alpha-bungarotoxin	hypothetical prote			œ.	nicotinic acetylch	acetylcholine rece			nicotinic acetylch	nicotinic acetylch					inicotinic acetylch		probable nicotinic	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch		nicotinic acetylch
ID	ACHUA7	A57175	JN0113	G02259	T01378	S68588	JH0173	T25671	T19862	T19622	A53956	A37040	860589	A24572	ACFFA1	S12359	ACFFA2	T09289	ACCH2N	B37014	A40110	S12899	B35721	A30992	ACBOA1	ACHUA1	ACFFNN	JH0174	JC4021
DB	-	~	~	~	~	7	~	~	~	~	7	7	~	N	-	N	-	7		~	7	~	~	7	Н		Н	7	7
% Query Match Length	502	502	502	502	. 502	498	511	461	542	260	503	. 502	495	499	267	557	276	464	528	512	511	200	495	517	457	457	521	503	627
& Query Match	47.7	47.6	47.5	47.4	47.2	46.9	46.5	42.9	41.0	40.9	37.5	37.2	36.8	36.8	36.5	35.8	35.7	35.2	35.0	34.8		34.5	34.5	34.3	٠	34.3	34.1	34.1	34.0
Score	1260	1255.5	1253	1252.5	1246.5	1237.5	1226.5	1132	1083.5	1081	989	982.5	970.5	970.5	964.5	944	943	929.5	924.5	919.5	919	910	909.5	906.5	906	905	901		897.5
Result No.		7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

9

Gaps

50;

Ouery Match 47.7%; Score 1260; DB 1; Length 502; Best Local Similarity 48.5%; Pred. No. 2.6e-99; Matches 247; Conservative 75; Mismatches 137; Indels 5

		nicotinic acetylch nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	protein F25G6.4 [i				
ACCHAN	S10505	ACCH4N S13872	A39218	A26456	G02421	S14703	A24383	I49458	ACCHNN	I50548	ACRYA1	A28529	S08162	E89134
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456	205	457	470	625	498	459	457	445	491	461	461	457	457	559
33.9	93.6	33.7	33.7	33.6	33.6	33.5	33.5	33.5	33.4	33.3	33, 2	33.2	32.9	32.7
968	895	168 8	890	888	887	885.5	882	883.5	881	879.5	876.5	875.5	869.5	862
30	31	3 G	34	35	36	37	38	39	. 40	41	42	43	44	45

## ALIGNMENTS

Richini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Helnemann, S. Genomics 19, 379-381, 1994 A;Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini A;Reference number: A54194; MUID:94245214; PMID:8188270 A;Accession: A44194 A;Accession: A44194 A;Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <chi>A;Cross-references: GB:223141; NID:9457736; PIDN:CAA80672.1; PID:9457737 A;Cross-references: GB:22141; NID:9457736; PIDN:CAA80672.1; PID:9457737 A;Cross-references: GB:2318751; OMIM:118511 A;Map position: 1594-1594 A;Note: defects in this gene have been associated with mental retardation and schizop C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains C;Superfamily: acetylcholine receptor alpha-7 chain, neuronal #status predicted <sig>C;Superfamily: acetylcholine receptor alpha-7 chain, neuronal #status predicted <tr25-280 #status="" <tr25-e372="" <tr25-e572="" <tr26-280="" acetylcholine="" alpha-7="" chain,="" domain:="" neuronal="" nicotinic="" predicted="" prod<="" product:="" production="" receptor="" th="" transmembrane=""><th>A; Cente: A; Cente: A; Cente: A; Cente: A; Map position: 15q14-15q14 A; Note: A; Complex: A; Complex</th></tr25-280></sig></chi>	A; Cente: A; Cente: A; Cente: A; Cente: A; Map position: 15q14-15q14 A; Note: A; Complex: A; Complex
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Oy 12 ALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQOIIDVDEKNQLLIT 71	OY 67 OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYOTN 126   1
72 NIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVV <sup>®</sup> RS 1	127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDOHCDMKFGSWTYDGNQLDLVLKDEAGGD
OY 132 GGSCLYVPPGIFKSTCKMDIAMFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDF1 191	Qy 187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
QY 192 TNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRTLYYFFNLIVPCVLISSMALLG 251	QY 247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWVAS 306
Qy 252 FTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLT 311	OY 307 SVVLTVVVLNYHHRTADIHEMPOMIKSVFLQMLPWILRMSRPGKKITRKTIMMNTRMREL 366
OY 312 VVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRWSRPGKKITRKTIMMNTRMRELELKER 371	Qy 367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRKS 417
QY 372 SSKSLLANVLDIDDDFRHGPPPNSTASTGNL	QY 418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCL 477
QY 413 DFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKRADEBAELLSDWKFAAM 470	Qy 478 FVFTLFTIATVAVLLSAPHII 499  ::     ::    ::   473 MAFSVFTICTIGILMSAPNFV 494
Qy 471 VVDRFCLFVFTLFTIATVAVLLSAPHII 499               ::        ::        : 	RESULT 3 JN0113 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
A57175 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse C;Specias: Mus musculus (house mouse) C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999 C;Accession: A57175 R;Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L. Genomics 26, 399-402, 1995 A;Title: Cloning and mapping of the mouse alpha?-neuronal nicotinic acetylcholine recept A;Reference number: A57175; MUID:95324936; PMID:7601470	-bungarotoxin-binding protein alpha chain (chicken) (a(chicken) (172; S28018; B25738; S26566 (d, D.; Matter, J.M.; Hernandez, M.C.; Bertrand tinic acetylcholine receptor subunit (alpha 7) (13; MuID:91097796; PMID:1702646
A;Accession: A57175 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-502 <orr></orr>	
A, Cross-references: GB:L37663; NID:q790853; PIDN:AAC42053.1; PID:g790854 C, Superfamily: acetylcholine receptor C, Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;	A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of t A;Reference number: JH0172; MUID:90315158; PMID:2369519 A;Accession: JH0172
status predicted  Alcholine receptor Status predicted Status predicted Status predicted	
F.396-317 Domain: transmembrane #status predicted <pr3> F.470-488/Domain: transmembrane #status predicted <pr4> F.470-488/Domain: transmembrane #status predicted <pr4> F.46.90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F.365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted F.445/Binding site: phosphate (Thr) (covalent) #status predicted F.442/Binding site: phosphate (Tyr) (covalent) #status predicted</pr4></pr4></pr3>	R.Matter-Sadzinski, L.; Hernandez, M.C.; Koztocii, T.; Ballivet, M.; Matter, J.M. EMBO J. 11, 4529-4538, 1992 A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter A;Reference number: S28018; MUID:93049204; PMID:1425587 A;Accession: S28018 A;Molecule type: DNA
Query Match 47.6%; Score 1255.5; DB 2; Length 502; Best Local Similarity 49.6%; Pred. No. 6.3e-99; Matches 249; Conservative 78; Mismatches 148; Indels 27; Gaps 7; Qy RAL-LALLPVSEQCHEKRLIANYNTLERPVANESEPLEVREGLTLQQIIDVDEKN 66 10 LALAAALLHVSLQGEFQRRLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN 69	A; Residues: 1-18 <mas. 1-18="" 1985="" 5208-5212,="" 82,="" <mas.="" a94055;="" a;="" acad.="" accession:="" acetylcholine="" and="" are="" b.m.;="" b25738="" b;="" barnard,="" bmbl:x68246;="" brain="" but="" conti-tronconi,="" cross-references:="" different="" dolly,="" dunn,="" e.a.;="" erythrocyte="" f.a.;="" gb:s49751;="" homolog="" j.o.;="" lai,="" leghorn;="" molecule="" muid:85270494;="" muscle="" n.;="" natl.="" nicotinic="" nid:g65319;="" number:="" pid:g65320="" pidn:caa48317.1;="" pmid:3860855="" proc.="" protein<="" ray,="" receptors="" reference="" residues:="" s.m.j.;="" sci.="" td="" title:="" type:="" u.s.a.="" white=""></mas.>

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VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
            Ouery Match
Best Local Similarity 48.45
Matches 249; Conservative
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C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha 7 neuronal nicotinic acetylcholine receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 C;Accession: G02259 R;Leonard, S. submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                             TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAMPPEDDQHCDMKFGSWTYDGNOLDLVLKD
|: |||:|| | | | | |:||||||:|::
|TFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFPFDVQKCNLKFGSWTYGGWSLDLQMQE
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Residues: 24-25,'ET',28-41,'X',43-45,'X',47 <CON>:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin
                                  80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                             Length 502;
                                                                                                                                                                                                        47.5%; Score 12.0., 48.8%; Pred. No. 1e-98; five 81; Mismatches 145; Indels
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A;Accession: G02259
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-502 <LEO>
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Matches 250; Conservative
                        C;Genetics:
A;Introns: 19/1; 65/3;
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                                                                                                                                                                       QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                     MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
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Riscassion: T01378
Riscapela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A;Title: Molecular cloning; functional properties, and distribution of rat b
A;Reference number: Z14310; MUID: 93147931; PMID: 7678857
A;Accession: T01378
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-502 <SEG>
A;Cross-references: EMBL: S53987; NID: 9264770; PIDN: AAB25224.2; PID: 95705903
A;Experimental source: brain
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic receptor alpha 7 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                             LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
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                                            51;
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    Length
                                            Indels
  5;
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                       .1e-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKERSSKSLLANVLDIDDDFRHGPPPPRSTASTGNL
; Score 1252.5;
; Pred. No. 1.1e-
74; Mismatches
  47.4%;
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Qy Db	187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRLLYYFENLIVPCVLISS 246 1	Qy	359 MNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPCS 408 : :
Oy Db	247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLALVAETLPQVSDAIPLLGTYFNCIMFWVAS 306 111   1   1   1   1   1   1   1   1   1	Qy	409 IFRTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELIS 463
oy Db	307 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366 	QQ Db	464 DWKFAAMVVDRFCLEVFTLFTIIATVAVLLSAPHII 499 
Qy Db	367 ELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIFRTDFRKS 417	RESULT JH0173	riedo Cardele aistos
Yo qa	418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKRADEBAELISDWKFAAMVVDRFCL 477	alpha-bun C;Species C;Date: 3 C;Accessi	ungarocoxin-binding process applies claim precessos es: Gallus gallus (chicken) 31.Dec.1991 #sequence_revision 31-Dec-1991 #text_chan sion: JH0173
Qy	478 FVFTLFTIATVAVLLSAPHII 499  ::      : :    : 473 MAFSVFTICTIGILMSAPNFV 494	R;Schoe Neuron A;Title A;Refer	Schoepter, R.; Conroy, W.G.; Wniting, P.; Gore, M.; Lindstrom, J.; Wn. Lindstrom, J.; Word 5, 35-48, 1990 Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of t Reference number: JH0172; MUID:90315158; PMID:2369519
RESULT	· ·	A; ACCE A; MOLE · A; Resi A; Cros	A:Accession: JH0173 A:Molecule type: mRNA A:Residues: 1-511 <sch> A:Cross-references: GB:X52296; NID:q63081; PIDN:CAA36544.1; PID:q63082</sch>
nicoti C; Spec C; Date	nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis e C;Species: Caenorhabditis elegans C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999	A; Exper A; Note: C; Comme	ce: brain ce is similar to acetylcholine receptor a ngarotoxin binding proteins are localized
C; Acce R; Ball J. Mol A; Title	ssion: S68588; S57496 ivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D. - Biol. 258, 261-269, 1996 e: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.	C; Supe C; Keyv C; Keyv F; 1-3(	etylcholine receptor  etylcholine receptor  gnal sequence #status predicted < alpha-bungarotoxin binding prote
A; Rere A; Acce A; Stati A; Molec	A; Kerefence number: SB838/; MUID:951964/8; PMID:852/024 A; Accession: S66588 A; Status: nucleic acid sequence not shown A; Molecule type: MRNA	F; 270- F; 304- F; 479-	239-26/Domain: Liminamentrane #status predicted <tm2> 270-288/Domain: transmembrane #status predicted <tm2> 304-323/Domain: transmembrane #status predicted <tm3> 479-496/Domain: transmembrane #status predicted <tm3> 6479-496/Domain: transmembrane #status predicted <tm3> 6479-496/Domain: transmembrane #status predicted <tm4> 6479-496/Domain: transmembrane #status predicted</tm4></tm3></tm3></tm3></tm2></tm2>
A; Resid A; Cross C; Supei C; Keywo	KeSIQUES: 1-498 <bal. Cross-traferences: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088 Superfamily: acetylcholine receptor Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;</bal. 	0uery Best L	Match 46.5%; Score 1226.5; DB 2; Length 511; ocal Similarity 46.6%; Pred. No. 1.9e-96;
F;1-19 F;20-4	:1-19/Domain: signal sequence #status predicted <sig> ;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <mat></mat></sig>	Matches	246; CONSEIVALIVE /5; MISMALCHES 134; INDELS /5; GAPS 5 LAALALLALLEVSEQQPHEKRLINALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE 64
Query Ma Best Loc Matches	Query Match46.9%; .Score 1237.5; DB 2; Length 498;Best Local Similarity 47.5%; Pred. No. 2.1e-97;Matches 245; Conservative 80; Mismatches 140; Indels 51; Gaps 9;	qa	
	2 APMLAALALLAVSEQGPHEKRLLNALLANVTLERPVANESEPLEVRFGLTLQQIID 61	QY	65 KNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQ 124    :        :           :         ::      ::
Oy Oy		Oy Dp	125 TNVVVRSGGSCLXVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG 184
Op Oy		QY	185 GDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI 244
Dp. Oy	122 TYQTNMIVYSTGLVHWVPPGIFKISCKIDIQWFPFDEQKCFFKFGSWTYDGYKLDLQP 179 182 EAGG-DLSDFITHGEWYLLGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240 11  : :      :: :   ::	Oy Db	245 SSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWV 304
do y	180 ATGGFDISEYISNGEWALPLTTVERNEKFYDCCPEPYPDVHFYLHMRRRTLYYGFNLIMP 239 241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300	QY	ASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRWR
g qa	:  :	අ	313 GLSVVVTVLVLQFHHHDPQAGKMPRWVRVILLNWCAWFLRMKKPGENIK 361 365 ELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIF 410
Οy	301 MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIM 358	Ş.	-  -

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අු	362 PLSCKYSYPKHHPSLKNTEMNVLPGHQPSNGNMIYSYHTMENPCC 406	G E-ILIVIAN
οý	GGLGSHHRELHLILR	T19867
qq	407PQN-NDLGSKSGKITCPLSEDNEHVQKKALMDTIPVIVKILEEVQFIAMR 455	4
oy.	452 MKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499	C;Date: 15-OCT-1999 #sequence_revision 15-OCT-1999 #text_change 18-Feb-2000 C:Accession: T19862 #sequence_revision 15-OCT-1999 #text_change 18-Feb-2000 B-Hembry C
qa	456 FRKODEGEEICSEWKFAAAVIDRLCLVAFTLFAIICTFTILMSAPNFI 503	submitted to the EMBL Data Library, March 1996 A; Reference number: 219188
RESULT T25671		A: Accession: T19862 A: Status: prefilminary; translated from GB/EMBL/DDBJ
hypothe	tical protein D2092.3 - Caenorhabditis elegans ss: Caenorhabditis elegans	A; Residues: 1-542 ANA A; Residues: 1-542 AND
C; Date: C; Acces	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 sion: T25671	
R;Gattu submitt	ng, S.; Maggi, L. ed to the EMBL Data Library, February 1997	A Gene: CESP:C40C9.2
A;Descr A;Refer	A; Description: The sequence of C. elegans cosmid D2092. A; Reference number: 220067	A.introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1 C.Superfamily: acetylcholine receptor
A; Acces A; Statu	sion: T25671 s: preliminary; translated from GB/EMBL/DDBJ	Query Match 41.0%; Score 1083.5; DB 2; Length 542;
A; Molec A; Resid	ule type: DNA les: 1-461 <gat></gat>	Similarity 42.6%; Pred. No. 3.2e-84; 2; Conservative 86; Mismatches 152; I
A; Cross A; Exper	<pre>Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3 Experimental source: strain Bristol N2; clone D2092</pre>	9 JOHEK RLLNALLANYNTLERPVANESEPLEVRFGLTLOOIIDVDEKNOLL
C;Genet A;Gene:	ics: CESP:D2092.3	
A; Map p	ositión: 1 	Qy 1TNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNV 12
C; Super		Db 77 TLVAWIEYQWTDYKLKWDPSEYGGIKDIRIPGNANAIWKPDVLLYNSADENFDSTYPVNY 136
Ouery Best	Query Match 42.9%; Score 1132; DB 2; Length 461; Best Local Similarity 44.7%; Pred. No. 1.9e-88; Matches 216; Conservative R6. Mismaches 1777, Indale 54. Cane 6.	Qy 128 VVRSGSCLXVPPGIFKSTCKMDIAMFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDL 187
»	NYNTLERPVANESEDI. EVBEGITIOOTIDVDEK NOTI. TRUIMI SI. FWNN 82	Db 137 VVSYTGDVLQVPPGILKLSCKIDITYFPFDDQICHLKFGSWTYSGNFIDLRINGPEGKNI 196
G qa		188 SDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRTLYYFFNLIVP
0y	83 NLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYOTNVVVRSGGSCLXVPP 140	197 SDEGIDVQYYVQNGEWNLLAVPARHETNIFDEQPYPSLFFYLIQRRTLYYGLNLIIP
QQ	86 KLQWEPKKYGGIQDIRFPGSSDHIWRPDVLLYNSAAEDFDSTFKSNLLTYHTGTVVWIPP 145	Oy 241 CVLISSMALIGETLEPDSGEKLILGYTILLSLIVFLMLVAEFLEPOVSDAIPLLG 294
ογ	141 GIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEW 196	295 TYFNCIMPMVASSVVLTVVVLNYHHRTADIHEMPOMIKSVFLOMLPMILÄMSRPGKKITR
qq		315 AFFSCCMLVVSASVVFTVLVLHNRKPETHEMSPFLRELLIWLPWLLLMRRPG
<b>상</b> 원	197 YLIGMPGKKNTITYACCPEPYUDVTFTIMIRRRTLYYPRILIYPCVLISSMALLGFTLPP 256 206 QVISTNAKRVVSYYKCCPEPYPVNYYLHIRRRTLYYGFNLIPSLLISLMALLGFMFPP 265	Oy 355 KTIMMUTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRT 412
٥٧		370 KTIFNCTHLKAEKAEEKAKQGSIKNGVGPGKPTDSVHPSEGLSLMKN
QQ		413DFRRSFVRPSTMED-VGGGLGSHHREL
Qy	317 YHHRTADIHEMPQWIKSVFLQWLPWILRWSRPGKKITRKTIMMNTRMRELELKERSSKSL 376	DD 4.17 IKLGRQQTIDFEFEFHVQHNHLMPVAPSEMTPRVTYSKVMAESYVEDVVMTELNKYMQKA 4/6
Dp	326 LHFRSADSHEMNPLVRRVLLEFLPWLLFMSRPGYKFVK363	4.35 BILLURELQTITATORNINEDERE TISUMERAMY VORCUER FILETITALY VALUES  [4   1     1
λο .	LANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGCLGSHHR	495 APHII 499
° 6	364 -ANVIDSTDKMPKKPKNPLDCNLPSNHAGYEAQIL	:  :    Db 537 SPHLI 541
දි සි	43/ ELHILLEKELÖYITAKMKKADEELISDWKFRAAMVORFCLEVFTLETIITATVAYLLSAP 496 	RESULT 10
ò	497 HTT 499	T19622 hunothatical protein Clius 3 - Caonorbanditic elegans
<i>5</i> 8	===	uypounettaal potemi Carna.a Caemormabortus eregams C;Species: Caemormabditis elegams C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 21-Jan-2000

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173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; eceptor
                                                                                                                                                                   SSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLL-----G 294
                                                                                                                                                                                                                                             YLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                        KSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDL 187
                                                                                                                                                                                                                                                                                                       TVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGP--GCSIFRT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAKQGSIKNGV-----GPGKP-----TDSVHPSEGLSLMKN 416
                                                                                                           VQHNHLMPVAPSEMTPRVTYSKVMAESYVEDVVMTELNKYMQKA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
ans
revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                 75;
                                                  %; Score 1083.5; DB 2; Length 542;
%; Pred. No. 3.2è-84;
86; Mismatches 152; Indels 75;
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A;Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R;Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990
A;Description: Nucleotide sequence of the mature human nicotinic acetylcholine recept A;Reference number: S21338
A;Accession: S21338
                                                                                                                                                                          A; Cross-references: EMBL: X53559; NID: g34985; PIDN: CAA37625.1; PID: g34986
                                                                                                                                                                                                                               GDB:125219; OMIM:118503
                                                                                                                                                                                                                              A;Cross-references: GDB:125219; OMIM::
A;Map position: 15q34-15q34
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                  Query Match 37.5%
Best Local Similarity 38.9%
Matches 202; Conservative
                                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 30-503 <ANA>
A; Residues: 1-503 <MIH>
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Richovilovic, M.; Roses, A.D.
Richovilovic, M.; Roses, A.D.
A; Mille: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal A; Reference number: A53956; MUID:91114756; PMID:1989896
A; Accession: A53956
A; Accession: A53956
A; Accession: A53956
A; Accession: Assays
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                                                                                                                                                                                                                                                                                                                                                                                                          80 NDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVVVRSGGSCLYVP 139
                                                                                                                                                                                                                                                                                                                                                                                                                              PGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLI 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTADIHE-MPQWIKSVFLQWLPWILRMSRP------GKKITRKTIMMNTRMR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: : :: | :::|:: | |||| :| | || || RSPEQYKPMNKFLKTLLLGWLPTLLGGGRAVLELSVHGAHYASDNKKKQRQYLIEVERH 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELELKERSSKSLLANVLDID-----DDFRHGPPPPNSTAST--GNLGPGCSIFRTDFR 415
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                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                  Length 560;
                                                                                                                                                                          A;Gene: CESP:C31H5.3
A;Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
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Pred. No. 5.5e-84;
8; Mismatches 155;
                                                                       GB/EMBL/DDBJ
                  Library, April 1997
                                                                     Status: preliminary; translated from
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                                                                                  A; Molecule type: DNA
A; Residues: 1-560 <WIL>
A; Cross-references: EMBL: 293778;
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TAIISYNAPHLFV 560
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           A; Reference number: Z19153
A; Accession: T19622
A; Status: .....
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 R;Kershaw, J.
submitted to the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal (version 2)
                                                                                                                                                                                                                                                                                                                                                                                       61 DVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                                                                                                                                                                                                                      GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL...--GPGCS---- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------IFRIDFRRSFVRPSIMEDVGG--GLGSHHRELHLILRELQFITARMKK 454
                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: A37040; S24592
Neurosci. Lett. 111, 351-356, 1990
A;Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subu A;Reference number: A37040; MuID:90245296; PMID:2336208
A;Reference number: A37040
A;References: EMBL:X52239; NID:g177897; PIDN:AAC84176.1; PID:g177898
                                                                                                                                                                                                                                                                    G-SSMNLKDYWESGEWAIIKAPGYKHDIKYNCCEEIYPDITYSLYIRRLPLFYTINLIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
                                                                                                                                                       181 DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TSNEGNAQKPRPLYGAELSNLNCFSRAESKGCKEGYPC
                                                               Gaps
                                                            62;
      Length 503;
37.5%; Score 989; DB 2; Length 50
38.9%; Pred. No. 3.3e-76;
tive 91; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 ADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLL 493
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C: Superfamily: acetylcholine receptor	
C.Neywolus: Neuroliansmiller receptor; transmembrane protein F;1-28/Domain: signal sequence #status predicted <sig>F;1-28/Domain: signal sequence #status predicted <sig>F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <mat></mat></sig></sig>	QY 65 KNQLLITNIMLSLEWNDYNLRWINSEYGGYKDLAITPNKLWKPDYLMYNSADEGFDGTYQ 124   ::  :  :  :  :  :  :  :  :  :  :  :
Query Match 37.2%; Score 982.5; DB 2; Length 502; Best Local Similarity 38.9%; Pred. No. 1.2e-75; Matches 199; Conservative 89; Mismatches 163; Indels 61; Gaps 5;	QY 125 TNVVVRSGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG 184   :::   ::
QY 8 LALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQ 67	QY 185 GDLSDFITNGEWYLIGNPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI 244 :
QY 68 LLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNV 127 ::   :	QY 245 SSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMV 304   :
Qy 128 VVRSGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDL 187 :::   ::	QY 305 ASSVULTVVVLNYHRTADIHEMPQWIKSVFLQWLPWILRMSRFGKKITRKTIMMNT 361   1   1   1   1   1   1   1   1   1
Qy 188 SDFITNGEWYLIGMPCKKNTITYACCPEPYVDVTFTIMIRRRILYYFFNLIVPCVLISSM 247	QY 362 RMRELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIFRTDFRRSF 418  1             1:1    DD 366 ELSNLNCFSRIESKVCKEGYPCQDGLCG-YCHHRRAKISNFSANL 409
Oy 248 ALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFNVASS 307 :	QY 419 VRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFC 476
OY 308 VVLTVVVLNYHHRTADIHEMPOMIKSVFLQMLPWILRMSRPGKKITRKTIMMNTRMRELE 367 : :	Oy 477 LEVETLETIATVAVLL 493  Db 470 LWVFILVCILGTAGLEL 486
QY 368 LKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCS 408 :	
QY 409IFRTDFRRSFVRPSTWEDVGGGLGSHHRELHLILRELQFITARMKKADEEAEL 461  1	nicotinic acetylcholine receptor alpha-3 chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996 C;Accession: A24572
Oy 462 ISDWKFAAMVVDRFCLFVFTLFTIATVAVLL 493	R.Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, S.; Patrick, Nature 319, 368-374, 1986 A;Title: Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholina. Reference number: A24572; MUID:86118671; PMID:3753746 A:Accession: A24572
RESULT 13 S60589 acetylcholine receptor alpha chain precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999	A;Molecule type: mRNA A;Residues: 1-499 <bou> C;Superfamily: acetylcholine receptor C;Superfamily: acetylcholine receptor C;Keywords: glycoprotein; ion channel: neurotransmitter receptor; postsynaptic membra F;1-25/Domain: signal sequence #status predicted <sig> F;26-499/Product: nicotinic acetylcholine receptor alpha chain #status predicted <mat< td=""></mat<></sig></bou>
Rictiado, M.; Alamo, L.; Navarro, A. Neurochem. Res. 17, 281-287, 1992 A;Title: Primary Structure of an agonist binding subunit of the nicotinic acetylcholine A;Reference number: 560589; MUID:92319195; PMID:1620271	Query Match 36.8%; Score 970.5; DB 2; Length 499; Best Local Similarity 39.6%; Pred. No. 1.2e-74; Matches 199; Conservative 91; Mismatches 180; Indels 33; Gaps 7;
A;Accession: S60589 A;Status: preliminary A;Molecule type: mRNA A:Residnes: 1-405	OY 3 PMIAALALLAUVSEQCPHEKRILMALLANYNTLERPVANESEPLEVREGITLQOIIDV 62
A; Cross-references: EMBL:X57032; NID:g297762; PIDN:CAA40348.1; PID:g297763 C; Superfamily: acetylcholine receptor C; Keywords: neurotransmitter receptor F; 1-21/Domain: signal sequence #status predicted <sig>F; 1-21/Domain: signal sequence #status predicted <sig>F; 70-405/Droduct: acetylcholics</sig></sig>	63 DEKNQLLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWRPDVLMYNSADEGFDGT
^II	123 YOTNOVYRSGSCLTVPPG-EKSTCKMDJAMFPEDDQHCDMRFGSWTYDGNQLDLVLKDE :  :::   :::   ::
matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps /; Qy 5 LAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE 64	OY 183 AGGDLSDFTHUREWYLLGMPGKKNITTACCPEPTYDVPTHIMIRRETLYFFNLLYPCV 242  1 :

410 PERSEYNRENAVERSCRIOKOGE  411 PERSEYNRENAVERSCRIOKOGE  412 PERSEYNRENAVERSCRIOKOGE  413 PERSEYNRENAVERSCRIOKOGE  414 OF FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  405 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  407 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  408 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  408 VINNETELMETHOUTICATAGLEL 490  409 A477  400 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  401 VINNETELMETHOUTICATAGLEL 490  402 A476  403 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  403 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  404 A477  406 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  407 A477  408 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  408 A478  408 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  408 A478  409 FEALLTRESSESTSVANVESIGNASPEIRANDEN AG7  400 A478  400 A77 A611 FILL FILL FILL FILL FILL FILL FILL FI	a o o o o		o o o o	
Db 368 Qy 395 Qy 437 Db 476 Qy 497 Db 536 Search complet		NTRMRELELKRESSKSLANVEDIDDDFRHGPP	X q a	
0y 395 0b 428 0y 437 0b 476 0y 497 0b 536 search complet Job time : 19.		- FSANLTRSSSSESVNAVLSLSALSPEIKEAIQSVKYIAENMKAQNVAKEIQDDWKYVAM VVDRPCLEVFTLFTIIATVAVLL 493	Z qq	
Oy 437 Db 476 Qy 497 Db 536 Search complet Job time: 19.	,	468 VIDRIFLWVFILVCILGTAGLFL 490	Qy	
QY 497  Db 536 Search complet Job time: 19.	SULT		oy (	
Db 536 SL 5 Search completed; Job time: 19.7131	coti Spec Date	ha-1 chain precursor on 31-Dec-1991 #text_	g &	
Search completed: Job time: 19.7131	Acce	ssion: S00381; A38801 Y, B.; Ballidet, M.; Spierer, P.	qa	: SL
mestions (1557 cmos)  Cross-references: 6B:08.07194; NID:97575; PIDN:CAA30172.1; PID:97576  Accession, 3380 cm.	Titl Titl Refe Acce	tinic acetylcholine receptors from Drosophila to 83626; PMID:2840281	Search c Job time	ompleted: August : 19.7131 secs
Residues: 1-567 (2022)  Residues: 1-567 (2022)  Residues: 1-567 (2022)  Roces serfectederes: BMLX.X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576  Roces Serfectederes: PMLX.X07194; PIDN:CAA30172.1; PID:g7576  Roces Serfectederes: PMLX.X07194; PERCENT.X07101; PID:g7576  Roces Serfectederes: PMLX.X07194; PERCENT.X07101; PID:g7576  Roces Serfectederes: PMLX.X07194; PERCENT.X07101; PERCEN	Resi Cros	PIDN:CAA30172.1; PID:9757		
Genetics:  Genetics: FlyBase: NACR-alpha-96Aa  Cross-references: FlyBase: Phymonomia  Rap position: 38 96A  Therons: Seferences: FlyBase: Phymonomia  Rap position: 38 96A  Introns: 373: 116/2; 310/2; 401/1; 499/3  Introns: 373: 116/2; 310/2; 330/2; 401/1; 499/3  Introns: 373: 116/2; 331: 106/2; 330/2; 401/1; 499/3  Introns: Assocytloholine receptor  Repwords: glycoprotain: an channel: neuroransmitter receptor; postsynaptic membrane; 12.240/Domain: stransmembrane status predicted carro. 12.240/Domain: transmembrane status predicted carro. 12.252/Domain: transmembrane status predicted carro. 12.252/Disulfide bonds: status predicted carro. 12.240/Domain: transmembrane status predicted carro. 12.240/Disulfide bonds: status bonds: status predicted carro. 12.240/Disulfide bonds: status bonds: status predicted carro. 12.240/Disulfide bonds: status bond	Resi Cros	cute type: mkna dues: 1-567 <bo2> s.references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576 : 538-Tyr was also found</bo2>		
Thirtons: 04/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3  Superfamily: acetylcholine receptor  Superfamily: acetylcholine receptor  1.21/Domain: signal sequence *status predicted *S16> 1.22-50/Domain: extracellular *status predicted *CMIP> 22-240/Domain: extracellular *status predicted *CMIP> 22-240/Domain: extracellular *status predicted *CMIP> 22-240/Domain: transmembrane *status predicted *CMIP> 22-250/Domain: transmembrane *status predicted *CMIP> 23-250/Domain: transmembrane *status predicted *CMIP> 23-250/Domain: transmembrane *status predicted *CMIP> 23-250/Domain: transmembrane *status predicted *CMIP> 23-51/Domain: transmembrane *status predicted *CMIP> 24-51/Domain: transmembrane *status predicted *CMIP> 25-51/Domain: transmembrane *status predicted *CMIP* 25-51/Domain: transmembrane *status predicted *CMIP* 25-51/Domain: transmembrane *status *st	Gene	tics: : FlyBase:nAcR-alpha-96Aa s-references: FlyBase:FBgn0000036		
1-21/Domain: Signal sequence #status predicted <sig> 22-56/Product: incofinic acetylcholine receptor alpha-like chain #status predicted <az2-240 #status="" <azm2="" domain:="" extracellular="" predicted=""> 22-256/Promain: transmembrane #status predicted <azm2> 240-264/Domain: transmembrane #status predicted <azm2> 240-250/Domain: transmembrane #status predicted <azm2> 306-325/Domain: transmembrane #status predicted <azm2> 310-325/Domain: transmembrane #status predicted <azm2> 32-225/Domain: transmembrane #status predicted <azm2> 32-223/Disulfide bonds: #status predicted <azm2> 32-223/Disulfid</azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></azm2></az2-240></sig>	Map Intr Supe	position: 3K 90A ons: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3 rfamily: acetylcholine receptor		
272-290/Domain: transmembrane #status predicted <tm2> 306-325/Domain: transmembrane #status predicted <tm2> 306-325/Domain: transmembrane #status predicted <tm3> 314-532/Domain: intracellular #status predicted <tm4> 514-532/Domain: transmembrane #status predicted <tm4> 515-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5</tm4></tm4></tm4></tm4></tm4></tm4></tm4></tm4></tm4></tm4></tm3></tm2></tm2>	1-21 22-5 22-2 22-2	/ Domain: signal sequence #status predicted <sig> 67/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted <m #status="" 40="" <ext="" domain:="" extracellular="" predicted=""> 64/Pomain: extracellular #status predicted <ext> 64/Pomain: transmembrane #status predicted <tmi></tmi></ext></m></sig>		
45,233/Binding site: carbohydrate (Asn) (covalent) #status predicted  22.223/Disulfide bonds: #status predicted  Query Match 36.54; Score 964.5; DB 1; Length 567;  Best Local Similarity 36.54; Pred. No. 4.8e-74;  Matches 198; Conservative 95; Mismatches 158; Indels 91; Gaps 9;  21 PHEKRLLNALLANYNTLERPVANESEDLEVERGLIDDVEKNOLLITNIWLSLEWN 80  21 PHEKRLLNALLANYNTLERPVANESEDLEVERGLIDVERGLITNIWLSLEWN 80  21 PHEKRLLNALLANYNTLERPVANESEDLEVERGLIDVERGNOLLITNIWLSLEWN 80  32 PDAKRLYDDLLSNYNTRLIRPVGNNSDRITVKMGLRLSQLIDVNLKNOIMTINVWEOGWN 82  33 PDAKRLYDDLLSNYNTRLIRPVGNNSDRITVKMGLRLSQLIDVNLKNOIMTINVWEOGWN 82  4 II	306- 326- 326-	290/Domain: transmembrane #status predicted <tm2> 325/Domain: transmembrane #status predicted <tm3> 513/Domain: intracellular #status predicted <im7> 532/Comain: intracellular #status predicted <im7></im7></im7></tm3></tm2>		
Duery Match  36.5%; Score 964.5; DB 1; Length 567;  Best Local Similarity 36.5%; Pred. No. 4.8e-74;  Best Local Similarity 36.5%; Pred. No. 4.8e-74;  Autches 198; Conservative 95; Mismatches 158; Indels 91; Gaps  21 PHEKRLIABLEANYNTLERPVANESEPLEVREGLTLQQIIDVDEKNOLLITNIWLSLEWN 80	,45,2 ;149-	33/Binding site: carbohydrate (Asn) (covalent) #status predicted 163,222-223/Disulfide bonds: #status predicted		
21 PHEKRILANYNTLERPVANESEPLEVREGITLQQIIDVDEKNQLLITNINLSLEWN	Quer Best Matc	y Match Local Similarity 36.5%; Score 964.5; DB 1; Length 567; Local Similarity 36.5%; Pred. No. 4.8e-74; hes 198; Conservative 95; Mismatches 158; Indels 91; Gaps 9;		
81 DYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVVRSGGSCLYVPP	<b>5</b> - O			
141 GIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDL-YLKDBAGGDLSDFIT  :    :    :	<b>5.</b> 0			
		GIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDL-VLKDEAGGDLSDFIT		

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ADIHEMPOWIKSVFLOWLPWILRMSRPGKKITRKTIMMNTRMRELELKERS 372
                                                                                           -----TASTGNLGPGC----SIFRTDFRRSFVRPSTMEDVGGGLGSHHR 436
                                                                                                  ----DID-----DDFRHG------
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August 13, 2003, 15:14:30 ; Search time 43.9474 Seconds (without alignments) 1809.483 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	H. virescens acety	H. virescens acety	D. melanogaster ac	Drosophila melanog	Drosophila melanog	Human neuronal nic	Neuronal nicotinic	Human PRO2145 prot	Nicotinic acetylch
SUMMARIES	1D	AAY50816	AAY50815	AAY50814	ABB60432	ABB63683	AAW44153	AAW09025	AAB24088	AAB82690
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& Query	Macch	100.0	68.3	6.09	59.5	48.6	47.7	47.7	47.7	47.7
9	arore	2640	1803.5	1609	1570.5	1283	1258.5	1258.5	1258.5	1258.5
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Wild-type human al	Human neuronal NAC	Human neuronal nic	V274T variant huma	Neuronal alpha-bun	Mutant human alpha	Mutant human alpha	Mutant human alpha	Neuronal alpha-bun	Caenorhabditis ele	Caenorhabditis ele	Neuronal nicotinic	Chimeric alpha7/5-	Human neuronal NAC	. Human neuronal nic	Drosophila melanog	Mature cell surfac	Human neuronal nic	•~	Human neuronal NAC	Human neuronal nic	Drosophila melanog	neuronal	Alpha 2 subunit of	Neuronal nicotinic	Human neuronal NAC	Human neuronal nic	Prostate cancer-as	Caenorhabditis ele	2		Modified acetylcho		-		Drosophila melanog
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AAB50012	82435	ABG70492	AAW69216	AAW12368	AAB50015	AAB50016	AAB50017	AAW12369	AAE12824	ABP96318	AAW09022	AAB50014	ABB82431	ABG70488	ABB61954	AAB50018	AAW44156	AAW09018	ABB82434	ABG70491	ABB62727	AAW44155	<b>AAR73966</b>	AAW09021	ABB82430	ABG31800	ABG61850	AAE12823	ABP96317	AA017243	AA017245	ABB08885	AAR07143	ABB62694	ABB61667
AAB!	ABB	ABG	AAM	AAM	AAB!	AAB!	AAB.	AAW	AAE	ABP	AAW(	AAB:	ABB	ABG	ABB(	AAB	AAW	AAW(	ABB	ABG	ABB(	AAW.	AAR	AAW(	ABB	ABG	ABG	AAE.	ABP	AAO]	AAO.	ABB(	AAR(	ABB(	ABB
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258.5	3.5	3.5	5.1	253	. 5	3.5	.5	5.5	080	080	5.5	5.5	5.5	5.5	943	942	.5	33	933	33	33		2.5	.5	.5	5.5	ر. ت	122	122	.5	115	115	.5	5.5	906
1258	1258	1258	1254	ï	1252	1248	1242	1226	1(	7	986	396	946	946	٠,	٠,	94(	J1	٠,	J,	J1	927	922	922	925	922	922	Ji	٥١	918	٥١	٥١	910	306	יט
10	11	15	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

DT 17-FEB-2000 (first entry) XX DE H. virescens acetyl-choline receptor protein from clone Hva7-2. XX Acetyl-choline receptor; insect; insecticide; screen XX No neurotransmission; plant protection agent; conductance; AChR. XX NX Heliothis virescens. XX PN DE19819829-Al. XX PF 04-MAY-1998; 98DE-1019829. XX PR 04-MAY-1998; 98DE-1019829. XX PR 04-MAY-1998; 98DE-1019829. XX PR 04-MAY-1998; 98DE-1019829. XX PR NAZ-4477. DR WPI; 2000-014207/02. DR WPI; 2000-014207/02.	Hva7-2. screening AChR.
XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from PT insects, used to identify potential insecticides -	tor from

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                          This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                                                             CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                  GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK
                                                                                                                                                                                                                                                                                                                                          DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. viescens acetyl-choline receptor protein from clone Hva7-1.
                                                                                                                                                                         DB 21; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetyl-choline receptor; nicotinic; insect; insecticide; neurotransmission; plant protection agent; conductance; l
                                                                                                                                                                                               Indels
                                                                                                                                                                         100.0%; Score 2640; DB 21;
100.0%; Pred. No. 5.8e-270;
ive 0; Mismatches 0;
         Page 22-23; 26pp; German
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                                                                                                                                                                                     Similarity
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSTMEDVGGGLGSH-----HRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRF
                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68:3%; Score 1803.5; DB 21; Length 496; 68.7%; Pred. No. 1.9e-181; ive 53; Mismatches 78; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
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Matches 347; Conservative
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N-PSDB; AAZ24476.
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DE19819829-A1
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                                                                                                           04-MAY-1998;
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413

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414 FRRSEVRPSTMEDVG--GGLGS------HHR------ELHLILRELQFITARMKKA 455
                                                                                                                                                                                        ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell is -
                                 SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMNTR
                                                   SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                 -----MRELELKERSSKSLLANVLDIDDDFRHG--PPPPNSTASTGNLGPGCSIFRTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
535 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                         DEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHIIV 500
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61.1%; Pred. No. 8.6e-157;
iive 44; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 8088
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Matches 319; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLALLPVSEQ----GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                  Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.;
                                                                                                                                                                 D. melanogaster acetyl-choline receptor protein from clone Da7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.9%; Score 1609; DB 21; 60.8%; Pred. No. 1.4e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example la; Page 12-14; 26pp; German
                                                               AAY50814 standard; Protein; 770 AA.
                                                                                                                                                                                                                                                                                                                                                         98DE-1019829.
                                                                                                                                                                                                                                                                                                                                                                                         98DE-1019829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oellers N,
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.8
Matches 319; Conservative
                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-014207/02.
N-PSDB; AAZ24475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adamczewski M,
                                                                                                                                                                                                                                                                                  DE19819829-A1.
                                                                                                                                                                                                                                                                                                                                                       04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
                                                                                                                                                                                                                                                                                                                      11-NOV-1999.
                                                                                                                                 17-FEB-2000
                                                                                                 AAY50814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
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                              RESULT 3
                                               AAY5081
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                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 498;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL30511) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 LVYGLGLLIMIPACAAGPHEKRLLHALLDNYNSLERPVVNESDPLQLSFGLTLMQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 MLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 AINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.6%; Score 1283; DB 22; 79.4%; Pred. No. 1.1e-126; tive 30; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229..256
/label= TMDl
/note≂ "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= TMD3
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462..487
/label= TMD4
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain"
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brain tissue; screening; NAChR; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "encoded by CTS'
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/note= "transmembrane
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label= signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 79.4
231; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLVLKDEAGGDLSDFITNGEWYLIGM-PGKKNTITYACCP-------EPYVDVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV
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                                                                                                                                                                                                                                              LQQIIDVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSA
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11-JUL-2000; 2000US-0614150
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ABB63683 RESULT

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                    408 SIFRTDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host recombinant eap, mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                                                                                                                                                                           nicotinic acetylcholine receptor; nAChR; neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids encoding nicotinic acetylcholine receptor sub-units screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                      Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                               KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                    47.7%; Score 1258.5; DB
48.6%; Pred. No. 9e-124;
tive 75; Mismatches 13
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                                                                                                                                                                                                                                    AAW09025 standard; Protein; 502
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Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                 09-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta MAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASVEMSAVA--------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
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                                                                                                                                                                                                                                                                                                                                                                    Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 502;
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48.6%; Pred. No. 9e-124;
tive 75; Mismatches 13
                                                                                                                                                                                                               INST BIOTECHNOLOGY IND ASSOC
318..461
/label= cytoplasmic_loop
                                                                                                                                                                                                                                                                           Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 80-81; 99pp; English.
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                                                                                                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             activity of the receptor
                                                                                                                                                                                                                                                                       Elliott KJ, Ellis SB,
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                                                       WO9420617-A2
                                                                                                                                38-MAR-1994;
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                                          407
          ISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLISA 246
                                MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                              SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL 366
                                                                                                                                         ------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
                                                                          SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                               SIFRTDFRRSFVRPSTMEDV - -GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                                      Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulant; antianglogenic; leukaemia; lymphoid malignancy;
neuronal disorder; glial disorder; astrocytal disorder; anglogenic;
hypothalamic disorder; glandular disorder; macrophagal disorder;
epithalial disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                               proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillan KJ,
ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL - - -
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                                                                                                                                                                                                       466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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                                                                                                                                                                                                                                                                                                                                                 Human PRO2145 protein sequence SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 61; Fig 58; 286pp; English.
                                                                                                                                                                                                                                                                                  AAB24088 standard; Protein; 502
99WO-US28313.
99WO-US30911.
2000WO-US00219.
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99WO-US12252.
99US-0141037.
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Wood WI;
                                                                                                                                          367 ASVEMSAVA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2000;
                                                                                                                                                                                                                                                                                                                           29-JAN-2001
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23-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
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                                                                                                                                                                                                                                                                                                                   PRO genes. Exemplary conditions or disorders to be treated with supplications or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblascomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC5836 and AAAC5836 and AAAC5836 to AAC5836 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                       one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO6199, PRO8199, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO1055, PRO1059, PRO1069, PRO1055, PRO1069, PRO1067, PRO1069, PRO1069, PRO2181, PRO23, PRO39, PRO8111, PRO1153, PRO1184, PRO1184, PRO1187, PRO1189, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                      those characterised by overexpression and/or activation of the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 502;
   present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9e-124;
; Mismatches 138;
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48.6%; Pred. No. 9e-1
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7;

51; Gaps

Length 502;

99 69 126

246

306

366 366 407 407 465

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Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; duug design; protein co-ordinate data; schizophrenia; Alzheimer; disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                           Disclosure; Page 252-254; 260pp; English.
             Nicotinic acetylcholine receptor alpha7.
                                                                                                                                                                                                                                  (TEWE-) STICHTING TECH WETENSCHAPPEN,
                                                                                       Location/Qualifiers
                                                                                                                                                                                                 09-FEB-2001; 2001WO-EP01457.
                                                                                                                                                                                                               2000EP-0200443
                                                                                                                                                                                                                     2000EP-0203810
(first entry)
                                                                                                                 171..173
                                                                                                                                    210..217
                                                                                                                                                                                                                                                             WPI; 2001-497071/54.
                                                                                                                                                                                                                                                Sixma TK;
                                                                                                                                                                      WO200158951-A2
                                                                                                                                                                                                                                                                                               schizophrenia
                                                                                                                                                                                                             10-FEB-2000;
                                                                                                                                                                                                                      31-OCT-2000;
15-0CT-2001
                                                                         Homo sapiens
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                                                                                                                                                                                                                                                Smit AB,
                                                                                             Region
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G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
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                                                                                                                                                                                10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN
                                                                                                                                                                                                                                                       QLLITNIWLŞLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                                                             127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
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                                                               47.7%; Score 1258.5; DB 22; Lengt
48.6%; Pred. No. 9e-124;
live 75; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL---
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                                                                                                                Conservative
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N-PSDB; AAC90380.
                                                                                          Local Similarity
                   502 AA;
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                      Sequence
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                                                                  Query Match
                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Water-soluble ligand-binding proteins derived from molluscs and analogue of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins derived from analogues of ligand-gated ion channels, their crystals, and their wase for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming multimers and are amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  been substituted. New drugs can be developed that selectively intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome, Alzheimer's disease, addiction to nicotine or schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "conserved ligand-binding region, residues
Tyr210, Cys212, Cys213 and Tyr217 are
essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AChBP determining solubility of the AChBP, in the same positions as in the AChBP, and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the essential amino acids of at least 1 of the conserved regions of an nAChB have been substituted for the corresponding amino acids, and preferably entire stretches have
                                                                                                                                                                                                                                                                                                                                               /note= "conserved ligand-binding region, residues
                                                                                                                                                                                                                                                                                                                                                                                                                           residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "conserved.ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Trp171 and Tyr173 are essential
                                                                                                                                                                                                                                                                                                                                                                             Trp108 and Tyr115 are essential
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2001WO-US50985. 2000US-0703951.

29-OCT-2001;

01-AUG-2002

01-NOV-2000;

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246
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                                                                                                                                                                                                                                                                                                                                                                                  QLLITHIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                               QVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHTN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
                                                                                                               The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nicotinic acetylcholine receptor; NAChR; drug screening; NAChR alpha7 subunit; receptor.
                                                                                                                                                                                                                                                                                                                         99
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          Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
                                                                                                                                                                                                                                                                                                                                        VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| :| |||| |:|||||::|||||:
ISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
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                                                                                                                                                                                                                                                                 Length 502;
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                                                                                                                                                                                                                                                                 DB 22;
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KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                               Score 1258.5; DE
Pred. No. 9e-124;
; Mismatches 13
                                                                                 Disclosure; Pages 61-63; 77pp; English.
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                                                                                                                                                                                                                                     502 AA;
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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nuclectides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVVVTVIVLOYHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 QVLTINIWLQMSWIDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIFRTDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                             beta subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   КЈ;
                                                                                                                                                                                                                                                            neuronal nicotinic acetylcholine receptors, useful for in vitro
screening of a drug substance in a test system specific for humans
                                                                                                                                                                   Elliott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 1258.5; DB 23; Lengt
48.6%; Pred. No. 9e-124;
ive 75; Mismatches 138; Indels
                                                                                                                                                                   ď
                                                                                                                                                                                                                                             Cell comprising nucleic acids encoding human alpha and
                                                                                                                                                                   Siegel
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                                                                                                                                                                   Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                         Examples; Page 130-131; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                   Claeps BO,
                                                                                                                                   (MERI ) MERCK & CO INC
                                                                                                                                                                                                  2002-698532/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 AA;
                                                                                                                                                                                                                  N-PSDB; ABV73248
                                                                                                                                                                   Gillespie A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250;
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This sequence is the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents. e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic
                                                                                                                                                                                          SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL 366
                                                                                                                                                                                                                                                    G-----RMACSPTHDEHLLHGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
                     LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTLMIRRRTLYYFFNLIVPCVLISS
                                                                                       MALLGFTLPPDSGEKLTLGVT1LLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                         SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                               SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                              ---GPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cance neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding variant of human alpha? nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKenna DG, Monteggia LM;
                                                                                                                                                                                                                           ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL-----
                                                                                                                                                                                                                                                                                                                                                                 466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                                                                     V274T variant human alpha7 nAChR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW69216 standard; Protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Fig 2; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gopalakrishnan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Touma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sullivan JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-377593/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV44687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9828331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAChRS). By contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                       nicotinic acetylcholine receptor; nNAChR; receptor; 7 subunit.
                                                                                                                                                                                                                       Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                Claim 101; Column 59-64; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harpold MM;
                                                                                                                      A
                                                                                                                  ABG70492 standard; Protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0938154.
93US-0028031.
93US-0149503.
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                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott KJ, Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-711528/77.
N-PSDB; ABS54875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 AA;
                                                                                                                                                                                                                                                           !uman; neuronal
!on flux; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                            US6440681-B1
                                                                                                                                                                                     06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1992;
08-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
466
                                                                                                                                                     ABG70492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nNAChR
                                                                                                                                                                                                                                                           Human;
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                                                                                  RESULT 12
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468 AAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                 28-SEP-1989;
                             04-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-----RACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
                                                                                                                                                                                                                    LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                        OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYOTN 126
                                                                                                                                                                                                                                              VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                                   69
      psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAchR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                          MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIFRTDFFRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
                                                                                                                                                                LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                        SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                                                                                                                                                ---GPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   ASVEMSAVA-------PPP---ASNGNLLY IGFRGLDGVHCVPTPDSGVVC
                                                                                                                                            51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic; ligand binding; ion channel.
                                                                                                                        Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuronal alpha-bungarotoxin binding protein alphal subunit
                                                                                                                                            Indels
                                                                                                                       47.5%; Score 1254.5; DB 19;
48.4%; Pred. No. 2.4e-123;
ive 75; Mismatches 139; I.
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                                                                                                                                                                                                                                                                                                                                                                              The alphal subunit (AAW1236B) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotcoxin binding protein (AABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 VDEKNQVLTTNIWLQMYWTDHYLQWNVSEYPGVKNVRFPDGLIWKPDILLYNSADERFDA
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                                                                                                                                                                                                                                                New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
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Pred. No. 3.5e-123;
                                                                                          STUDIES
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89US-0413947
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Best Local Similarity 48.8
Matches 250; Conservative
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408 G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a mutant human alpha? nicotinic acetylcholine gated ion channel. The human alpha? ion channel was used in the construction of an alpha?/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha?/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
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5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
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llarity 48.4%; Pred. No. 3.9e-123;
Conservative 75; Mismatches 139;
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Claim 100; Pages 70-72; 77pp; English.
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N-PSDB; AAC90385.
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Description	B6632919 GH16126.3 A1292581 GH15518.5 AL530299 AL530299 AK034228 Mus muscu
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ssult No. Score	423.8 331.2 301.2 293.2
Result No.	U 7 8 4

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Sax: 510 48/6 fvy.
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or

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AK08115 AK08125 AK08174 AK05174 AK05173 AK08041 AK08047 AK08047 AK08047 AK08047 AK08047	BX437801- BU7702422 BU7702422 BU73068 BX403124 BX403124 BX711715 CA326954 BQ720344 CA751482 CA751482 CA374163 BI516733 BI516733 CB244163	CNSO3TC CNSO3TC CNSO901 CNSO901 AKO121 AKO1049 BC39916 CNSO06F BC40404 BB63769	
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240 240 240 293.2 240.2 240 240 239.2	236.8 2284.8 2228.2 2228.2 2220.4 210.6 210.4 200.2 202.2 202.2 201.8 199.2 199.2 198.8 193.8	7779 88 88 88 88 8 8 8 8 8 8 8 8 8 8 8 8	BGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
29788788788	2333308782828283838383838383838383838383838383	*59780010#45	RESULT 1 BG632919/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003511: arm.X [18792641.19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row. C column: 2 High quality sequence stops: 784.
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/db_xrefe"taxon:7227"
/clone="GH16126"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_l: EcoRI; Site_2;
XhoI; Sized fractionated cDNAs were directly ligated into pOT2.
Plasmid_CDNA library."
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                                                                                                                                                                                                                                                                                                                               Length 885;
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                                                                                                  1. .885
/organism="Drosophila melanogaster"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                            Score 423.8; DB 10;
Pred. No. 2.2e-106;
); Mismatches 262;
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                                                                                                                                                                                                                                                                                                                            28.2%;
68.9%;
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G07 bp mRNA linear EST 23-APR-2001
G185518.5prime GH Drosophila melanogaster head port2 Drosophila
melanogaster cDNA clone G115518 5 similar to CG4128: FBan0004128
'ion_channel' located on: 2L 3001-30E1;: 04/10/2001, mRNA sequence.
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                                      TACTCAATTACCACCATGGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAG
                                                                                                                                                                                 11 TGTTGGCGGCCTTTGGCGCTGCTTTGCTGCCGTATCGGAGCAAGGTCCTCACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA One Cyclotron Rd, Berkeley, CA 94720, USA Exa: 510 486 6798
Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu hit genomic AE003626: arm:2L [9617316, 9882551]
estimate-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 607)
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/organism="Drosophila melanogaster"
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Pred. No. 1e-80;
0; Mismatches 1
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Contact: Stapleton, M.
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Drosophila melanogaster
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al Similarity 76.7%;
405; Conservative
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KEYWORDS
SOURCE
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Query Match 20.0%; Score 301.2; DB 9; Length 1201; Best Local Similarity 60.2%; Pred. No. 3e-72:	7; Conservative 10; Mis	Qy         65 ACGAGAAGAGACTCCTGAACGCGTTGCTGCCGAACTACAACACCTGGAGCGACCGGTGG 124           :	0y 125 CCAACGAGGGGAACCGCTAGAGGTTCGGCTTGACCTTGCAGCAAATCATTGACG 184	Oy 185 TGGACGAGAAGATCAACTACTATAACCAATATGTGGCTGGGGGGGATGACT 244	Qy 245 ACAACCTGAGGTGGAACGACGAGGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCA 304	Oy 305 ACAAGTTGTGGAAGGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGA 364	Oy 365 CCTACCAGACCAACGTGGTGGTGGAGGGGGGGGGGTTGCCTGTACGTGCCACCTGGGA 424	425 TATTCAAGAGCACATGCAAGATGGGCGTGGTTCCCTTCGACGACCAACAGTGGCTGTG	QY 545 AGGCAGCGGCGATCTATCGGACTTCATAACAAATGGGAGTGTATCTAATAGGAATGC 604	Oy 605 CAGGCAAAAAGAACACAATAACATACGGGGGCCCGGAGCCCTACGTGGACGTCACCT 664	OY 665 TCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTACACCTGATCGTCGGGG 724	Oy 725 TGCTGATCTCATCGATGGCACTCCTGGGCTTCACACTGCCACCAGGACTCCGGGGAGAA 782	Oy 783 ACTCACACTTGGAGTCACTATTCTTCTATGGCTGATGCTGCTCAACCTGGTAGCCGA 842	OY 843 GACCCTGCCACAGGTCTCCGACGCTATCCCCTGTTAGGGACGTACTTCAATTGCATCAT 902	Qy 903 GTTCATGGTAGCTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCAC 954	RESULT 4 AK034228 LOCUS LOCUS DEFINITION Mus musculus adult male diencephalon CDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
131 AGAGCGAACCGCTAGAGGTCAGGTTGACCTTGCAGCAAATCATTGACGTGGACG 190	195 AATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCGGGAGGATCATCGACGTGGACG 254	191 AGAAGAATCAACTACTTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACC 250	251 TGAGGTGGAACGACAGGGGGTTATGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGT 310 	311 TGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC 370 	. 371 AGACCAACGTGGTCAGAAGCGCGCGCAGTTGCCTGTACGTGCCACCTGGCATATTCA 430	431 AGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCACACTGTGATGA 490 	491 AGTICGGTAGCIGGACAFAIGACGCAAICAGTIGGAICIGGIGCTAA 538 	AL530299 LOCUS AL530299 LOCUS AL530299 LOCUS AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA Clone CSODD007XP05 5-PRIME, MRNA sequence.	AL530299.2 GI:31068132 EST. Homo sapiens (human) M Homo sapiens	Eukaryota; metacoa; cnoidata; craniata; vertebrata; buteleostomi;  REFERENCE 1 (bases 1 to 1201)  AUTHORS Li,W B., Gruber,C., Jessee,J. and Polayes,D.	JOURNAL Unpublished  MMENT On Feb 13, 2001 this sequence version replaced gi:12793792.  Contact: Genoscope		<pre>u_rvsion or invitogen. fints sequence belongs to sequence cluster 7646.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODDO07CH03QPl&amp;cluster=7646.r. Contact :</pre>	reng Llang Enall: Illang@ilfetech.com URL: http://fulllength.lnvitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODD007CH03QPI. Location/Qualifiers	/orice /organism="Homo sapiens" /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	/clone="CSDD000TPOPS" /tissue_type="NEUNOBLASTOMA COT 50-NORMALIZED" /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="lib="lib="homo sapiens" NEUROBLASTOMA COT 50-NORMALIZED" /note="lib="lib="lib" sapients"/ lib" sapiens /note="lib" sapiens lib" sapiens lib

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VTLCISVLLSLTVFLLITEIIPSTSIVIPLIGEYLLETMIFVTLSIVITVFVLMVH
RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIESMHKMANAPRFWPEPES
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                                                                     Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Poshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSEGGEK
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLKWFIIVCLLGTVGLFLPPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AGAGCGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 4 (MGD|MGI:87888, GB|NM_015730, evidence: BLASIN, 99%, match=1946)
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rakeda,r., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                       URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
Fax:81-45-503-9216)
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Pred. No. 7.4e-70;
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55.9%;
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                                                                                                                                                                                                                                                                                                                                             curinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T.; Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Mishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaqi, K., Yohyiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yohazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 565-573 (2002)
6 (bases 1 to 2940)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                                                                                                                                     Sciurognathi; Muridae; Murinae; Mus.
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Nature 409 (6821), 685-690 (2001)
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Sciurognathi; Muridae; Murinae; Mus
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Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning

AUTHORS TITLE REFERENCE

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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,R., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer according pipeline with 384 multicapillary sequencer School B. D. 1076861
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Analysis of the mouse transcriptome based on functional annotation of for full-length cDNAs

Nature 420, 563-573 (2002)

E (Dases I to 3230)

E (Dases) Lo 3230)

E (Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kaya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Satico, R., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Satico, R., Satico, H., Sakai, C., Sakai, K., Sakazume, N., Sanau, Y., Tanaka, T., Tana
Itoh, M., Konno, H., Okazaki, Y., Mayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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AKO81254

Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030030P04 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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Sciurognathi; Muridae; Murinae; Mus
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High-efficiency, full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
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SSCSIDVTFFPFDQQNCTMKFGSWTYDKAKIDLVSMHSRVDQLDFWESGEWVIVDAVG,
TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHH
RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIESMHKMANAPRFWPEPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
PTGSPASLKTRPSQLPVSDQTSPCKCTCKEPSPVSPITVLKAGGTKAPPQHLPLSPAL
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                                                         Research Group in Riken
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            Fax:81.45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Rike
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; cholinergic recendication; alpha polypeptide 4 (MGD|MGI:87888, GB|NM_015730, evidence: BLASTN, 99%, match=1946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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Pred. No. 7.8e-70;
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                                                                                                                                                                                                                 1. .3230
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        992 c
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Best Local Si
Matches 578;
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/dev_stage="adult"
1. .3483

    3483
    Anote-"cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891, GB|NM_009602, evidence: BLASTN, 998, match=1498)
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    1014 c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 CTGGCTGACCCAGGAGTGGGAAGATTATCGCCTCACATGGAAGCCTGAGGATTTCGACAA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 CAGTIGCCIGIACGIGCCACCIGGCAIAITCAAGAGCACAIGCAAGAIGGACAICGCGIG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 GTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGTAGCTGGACATATGACGCCAA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAATCAACTACTTATAACCAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 GGTCAAGGACCTCAGGATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 3483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 281.6; DB 1
57.7%; Pred. No. 1.3e-66;
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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hes 547; Conservative
                                                                                           .3483
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai,J., Shinagawa,A., Shibata;K., Yoshino,M., Itoh,M., Ishii,Y.,
Alzawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Alzawa,T., Ishi,K., Kiyosawa,H., Komdo,S., Yamanaka,I.,
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischman,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
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Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fulita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Ring,B., Kingwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-Oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
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PASMQGLAGAFQAEPAAAGLGRSMGPCSCGLREAVDGVRFIADHMRSEDDDQSVREDW
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KKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
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/de_stage="12 days embryo"
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H. Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
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Please visit our web site for further details.
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/db_xref="FaNTOM_DB:C530044P16"
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                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                               GGTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATC
        GGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTT
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HTC 05-DEC-2002

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RESULT 8 AK051742 LOCUS

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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:Dl30070121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence. AK051742
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
6 (bases 1 to 4046).

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaqaki,T., Hara, Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
21085660
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High-efficiency full-length cDNA cloning
weth. Enzymol. 303, 19-44 (1999)
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Mus musculus O day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279233
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                                                                                                                                                                  Submitted (16-70L-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Iaboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Rintep://genome.gsc.riken.go.jp/, Tel:81-45-503-922, CBN 11brary was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /DOCUMENT 16="BAC34749.1"
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STYVDITYDFIIRRKPLFYTINLIIPCVLITSLALLVFYLPSDCGGEKKKTLCISVLAL
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VKVVFLEKLPTLLFLQQPRHRCARQRLRLRRRQREREGAGTLFFREGPAADPCTCFVN
PASMQGLAGAFQAEPAAAGLGRSMGPCSCGLREAVDGVRFIADHMRSEDDDQSVREDW
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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saitoh,H., Sakai,C., Sakai,R., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinaqawa,A., Shiraki,T., Soqabe,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match*1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGG
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1127 c 1077 g 964 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/strain="c57BL/6J"
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/clone="p130070121"
/tissue_type="spinal ganglion"
/clone_lib="RIKEN full-length enr:/dev_stage="12 days embryo"
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nicotinic, beta polypeptide 2 (n
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57.7%;
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MRVPAEKIWKPDIVLYNNADGDEQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
PETYQDITWRKEGWSYDKAK TDLVLICASMMILKDVWESGEMATIKAPCYKHEIKYNCC
EETYQDITYSLYIERLEFYTULLIPCLLISFLYUVPYLBSDCGEKYTLCISVLLS
LTVFLLVITETIPSTSLYIPLIGEYLLFTWIFVTLSIVITVFVLNVHYRTPTTHTWPT
WYAYAVLLICENWEWTRYFTSEEDARTRNRFYGAELSALLWFSRADSKSCKEGYPCQ
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AQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BaC35404.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 CAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 GGCTAACGTGTCCCCATCCTGTCATCCAGTTTGAGGTGTCTATGTCTCAGCTGGTGAA 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATGACAAAACCAAAGCTCTACTCAAGTACACAGGAGAAGTGACTTGGATCCCTCCGGC 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGCCCCTATGTTGGCGGCCTTGGCGCTGCTGCTGCTGCTGCCCGTATCGGAGCTCC
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                                                    Please visit our web site for further details
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0; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                        /db_xref="FANTOM_DB:E130103E14"
/db_xref="taxon:10090"
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                                                                                        URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/qualifiers
1. .1864
                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="E130103E14"
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                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

E (bases I to 1864)

Adachl, J. Alzawar, K. Akimura, T., Hara, A., Hashizume, W., Hayashida, K., Hayata, N., Haramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayashida, K., Hayata, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawal, J., Kojima, Y., Kondo, S., Kouno, H., Kouda, M., Katoh, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Ohsato, N., Okazaki, Y., Salto, R., Salto, R.,
prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoliwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer canalysis (RISA) system-384-format
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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Radchi, J., Aizawa, K., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hangaki, T., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okzaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakati, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Yasunishi, A., Takaku-Akahira, S.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SEIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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3126 bp mRNA linear HTC 05-DEC-2002
MUS musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:47300/0744 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegani,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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                                                                                                                                                                                                          CCTGCTCATCTCCATCTGCACTGTGCTCTCTACCTGCCCTCCGACTGTGGGGAGAA 966
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                                                            787 CCCGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAGACATCAC
                                                                                                                                               GTACTCGCTATACATTCGCCGCCTGCTGTTCTACACCATCAACCTCATCATTCCGTG
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                                                                                                      CTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCGTG
                       GCCAGGCAAAAAGAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGACGTCAC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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/protein_id="BAC34740.1"
/db_xref="C1:26342156"
/db_xref="G1:26342156"
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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
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EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
LTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNNYRTPTTHTMPT
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AOWYNEIQDDMKYVAMVIDRIFLMVFILVCILGTAGLFLQPLMARDDT"
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                                                                                    enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                 /dev_stage="12 days embryo"
170. 1669
/note="unnamed protein product; NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471,
evidence: FASTY, 99.8%ID, 100%length, match=1497)
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACAACCTGAGGTGGAACGAGCAGCAGTATGGCGGGGGTCAAGGACCTCAGGATCACGCC
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/db_xref="FANTOM_DB:D130068A06"
/db_xref="taxon:10090"
/clone="D130068A06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 275.6; DB 1
Pred. No. 5.8e-65;
                                                            /tissue_type="spinal ganglion"
/clone_lib="RIKEN full-length
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HTMPTWYKAVFLNLLPRVMFMTRPTSTEEDAPKTNFYGAELSNLNCFSRADSKSCKE
GYPCODGTCGYCHHRYKISMFSANITRSSSBSVDAVLSLSALSPETKEALOSVKYI
AENMKAQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
                                                                                                                                                                                                                                           YNEIIRPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWKPSDY
QGVEFMRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI
DVTYFPFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEI
                                                                                                                                                                                                               /translation="MRSSDMGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATATICAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTG 482
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ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99 8%ID, 100%length, match=1497) putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TCACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AGCTGAGCACCGCCTGTTCCAGTACCTGTTTGAAGATTACAACGAGATCATCGGCCGGT
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Pred. No. 6e-65;
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                                                                                                                                       /protein_id="BAC37909.1"
/db_xref="GI:26348539"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative"
3126
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                                                 Kawai, J. Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Saito, T., Saito, R., Saito, T., Saoto, T., Sasvant, T., Saito, R., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Relischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pescole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuho, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolunga, N., Garninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashio, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ring, B., Ringyaz, L., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Marashizaki, Y., Rawajl, H., Kohtsuki, S., Rawajl, H., Kohtsuki, Y., Rawashizaki, Y., Rawashiza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Fax:81-45-503-9216)
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/db_xref="taxon:10090"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                             ACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGA
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                                                                                                                                                                                        843 GACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCAT
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Quackenbush, J., Schriml, L., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washlo, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Wagner, L., Washlo, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Hill, D., Marchionni, L., Mashluma, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
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/clone_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2010)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Group in Riken
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Hayashida,K., Hayatsu,N., Hiramcto,K., Hiraokay,T., Hirozane,T.,
HOTi,F., Imclani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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Encyclopedia Project of Genome Exploration Research Group in R
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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Matsuo, Y., Nikaido, I., Pesole, G.,
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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295 ATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGGTGACGAGGGT 354

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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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                                                                                                                                                                                                                                        535 CTAAAAGATGAGGCAGGCGGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTA 594
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ATCCCATCTGAACTCATCTGGAGGCCTGACATCGTCCTCTACAACAACGCGGACGGGAC
                                                   421 AGCATGCACAGCCGTGTGGACCAACT---GGACTTCTGGGAAGTGGGGAGTGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                GACGTCACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATC
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                                 TTTGACGGGACCTACCAGACCAACGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTG
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High-effictency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishli, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Codolouri, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Rabburner, M., Batalov, S., Casavant, T., Radota, K., Matsuda, H., Rasukawa, T., Saito, R., Kuchi, P., Lewis, S., Matsuo, Y., Mikaido, I., Pesole, G., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Brownstein, M.J., Bult, C., Carninci, P., Genaldo, M., Browstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, M. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K., Wangika, Y., Kamiya, M., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y., Yanga, Y., Kawaji, H., Kohtsuki, S., Mazaki, Y., Kawaji, H., Kohtsuki, S., Masaki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., Maraki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., Maraki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., Maraki, Y., Kawaji, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., Maraki, Y., Kawaji, H., Kawaji, H., Kawaji, H., Kawaji, Y., Kawaji, Y., Kawaji, H., Kawai, H., Kawa
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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R dachl,J., Alzawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hangaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiracka,T., Hurozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakawai,J., Kohina,Y., Kondo,S., Konno,H., Sakai,G., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shirati,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M., and Hayashizaki,Y., Toyay,T., Yasunishi,A.,
Sumi, N., Ishli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Nokazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,
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Encyclopedia Project of Genome Exploration Research Group in Riken
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Nature 409 (6821), 685-690 (2001)
21085660
11217851
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Fax:81-45-503-9216)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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908 bp mRNA linear EST 03-SEP-2002 AGENCOURT_8443358 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192234 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               984 TCGCCCAGCACCCACATCATGCCCGAGTGGGTGCGGAAGGTTTTTATCGACACTATCCCA 1043
                                                                    AAACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCC 840
                                                                                                                                                                                                                                      ATGITCATGGTAGCGTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCACCATCGA 960
                                                                                                                                                                                                                                                                                                                                                                                                                              GAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATC 900
624 CGGGGCTGGAAGCACTGGGTGTTCTACTCCTGCTGCCCCACCACTCCCTACCTGGACATC 683
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_l:
Not1; Site_l: Sali; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                TGCGTGCTGATCTCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAG
                                            ACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       рe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM13593 row. column: 19
High quality sequence stop: 598.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6192234"
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TITLE
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COMMENT
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BU149265
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/db_xref="G1:36325166"
/db_xref="G1:36325166"
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/dev_stage="0 day neonate"
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KSAIEGVKYIAETMKSDQESNNAAEEWKYVAMVMDHILLGVFMLVCLIGTLAVFAGRL
                                                                                                                                                                                                                                                                                                                                                                                          NCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKEARGWKHWVFYSCCPTTPY
LDITYHFVWQRLPLYFIVNVIIPCLLFSFLTSLVFYLPTDSGEKMTLSISVLLSLTVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGAGAAGAGCTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 TACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 AACAAGTIGIGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 GAAAAGATCTGGCGGCCGGACGTCGTTCTATAACAACGCAGCGAGCTTTGCCATT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 ACCTACCAGACCAACGTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 ATATICAAGAGCACATGCAAGAIGGACATCGCGTGGTITCCCTTCGACGACCAACACTGT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAACGAGAGCGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAATCATTGAC 183
                                                                                                                                                                        /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCAGGCGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATG
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Pred. No. 1e-56;
0; Mismatches 438; Indels 6;
  /strain="C57BL/6J"
/db_xref="FANTOM_DB:4831406G09"
/db_xref="taxon:10090"
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                                                                    /clone="4831406G09
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Best Local Similarity 54.6%;
Matches 535; Conservative
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5'-GACTAGTTCTAGATCGCGGCGCGCCT(15)-3'. Size selected > Lb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Fechnologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies. Technologies. 247 g 212 t
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                                                                                                                                                                                                      GGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAG 152
                                                                                                                                                                                                                                                               GTTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAGAATCAACTACTATAAAC 212
                                                                                                                                                                                                                                                                                                                                                                             231 CTTCTCCCTGAGCCTCCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAACCAC 290
                                                                                                                                                                                                                                                                                                                                                             CAATATATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTA 272
                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTAT 332
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                                                                                                                                                                                    33 GGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGAAGAGACTCCTGAACGCGTTGCT 92
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                                                                                                                                                            10;
                                                                                                                              Length 908;
                                                                                                                                                           0; Mismatches 275; Indels
                                                                                                                              Score 240; DB 13;
Pred. No. 2.7e-55;
                                                                                                                              16.0%;
60.4%;
                                                                                                                                            al Similarity 60.4
435; Conservative
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Copyright (c) 1993
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New nucleic acid encoding a nicotinic acetylcholine receptor from

PT

Drosophila melanog D. melanogaster ac Human PRO2145 nucl Wild-type human al

ABL13733 AAZ24475 AAC58395 AAC90380 AAT48239

1509 1509 1876

22 22 22 23 24 25 25 25

100.0 38.3 38.3 28.6 27.4 25.1 24.9

575 430.6 411.4 377.2

1503

AAZ24476 AA224477

Neuronal nicotinic

H. virescens acety Drosophila melanog

H. virescens acety

	6	73			1590	19	AAV44687	V274T variant huma
	10	73			1876		AAV12197	Human neuronal nic
	1;	2 5			18/6		ABV/3248	neuronal
	7 -	. t			0/07		ABS340/3	Multant human alaha
	14	75			1509		AAC90386	Mutant human alpha
	15	2			1509		AAC90387	Mutant human alpha
	16	63			1964		ABZ11298	Human polynucleoti
	17	342.4			2769		AAT59196	Neuronal alpha-bun
	9 7	96			1017		AAT5919/	Neuronal alpha-bun
	50	25			1869		ABL54794	Modified hen ACR s
	21	04			2082		AAT59527	Alpha4 subunit of
	22	04			3496		AAT48237	Neuronal nicotinic
	23	200			1809		AAS91552	DNA encoding novel
	4 در م	30			1908		AAT39328 AAT48236	Alpha4 Subunit Of Neuropal picotinic
	52	22			2277		AAV12199	Human neuronal nic
	27	02			2277		AAQ90387	Alpha 2 subunit of
	28	02			2277		ABV73243	Human neuronal NAC
	2 2	200			1177		ABS548/0 AAT48235	Human neuronal nic
	3.5	200			2664		ABK92165	Prostate cancer-as
	32	95		. 0	1896		AAL45870	Modified acetylcho
	33	95	19	. 9	1896		ABL54791	Modified hen ACR s
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	36	~ 6		4.0	1896		AAL4586/	Modified acetylcho
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	40	א כו	161	າຕ	2363		AAV12196	neuronal
	41	290	19	m	2363		ABV73245	neuronal
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DE	Ξ.	virescen	S	cetyl	-choline		receptor DNA from	clone Hva7-2.
X X	Ace	tyl-chol	oline	recel	Ä	nico	ic; insect;	icide;
KW	neu	rôt	ß	Ċ	plant	5	gent;	nce; AChR; ds.
yy OS	Hel	Heliothis	s virescen	cens				
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GAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATC
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                                         This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransanission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                          Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;
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identify potential insecticides
                                                                                                                                                                                                               Score 1503; I
Pred. No. 0;
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                       26pp; German.
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Matches 1503; Conservative
                       Claim 1a; Page 19-22;
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                                                  ACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACC
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                                                                                                                                                    0 or more cell-cell
                                                                                                                                                                                                                                                                                                                                               from WIPO
                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC
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                                                                                                                                                                                                                                                                             insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                    detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 1540;
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Pred. No. 8.7e-151;
0; Mismatches 394;
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les 977; Conservative (
                      2000US-191637P.
2000US-0614150.
23-MAR-2001; 2001WO-US09231
                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
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                                     ACGTATCCAACGAACGTGGTGGTGCGGAACAACGGCTCGTGTCTGTACGTGCCGCCCGGC
                                                                          ATATTCAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGT
                                                                                              GATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission (I) also vectors containing it, interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies protection against (I) encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 TACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 ATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCACCC
                                                                                            Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid encoding a nicotinic acetylcholine receptor from ects, used to identify potential insecticides
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                                                           DNA from clone Hva7-1.
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                                                                                                                                                                                       Location/Qualifiers
335..1825
/*tag= a
/product= "acetyl-choline receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 575; DB 21;
Pred. No. 1.9e-150;
0; Mismatches 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schulte T;
                                                           virescens acetyl-choline receptor
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llarity 64.6%;
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                                                                                                                                                       Heliothis virescens.
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                     17-FEB-2000
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 247 CAACTGCTTATAACGAATATTTGGCTCAAATTGGAATGGAACGATATGAATCTTCGATGG 306
                                                                                                                                                                                                                                         CTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAAACAAC
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                           AACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCCAACAAGTTGTGGAAG
                                                                               CCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAAC
                                                                                                                                                                                                                                                                                                              607 ATTCTAGCTTTATAACCAATGGGGAATGGGACTTGTTAGGTGGCCGGTAAACGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACA
                                                                                                                                                                                      439 TGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGT
                                                                                                                                                                                                     screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acetyl-choline receptor; nicotinic; insect; insecticide; scree neurotransmission; plant protection agent; conductance; AChR;
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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTTGGCGCTGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGAAGACTC
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                                                                                                                                                          Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681
                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                  pharmaceutical; gene; ss
                                                                                                                                                                                                                            Drosophila melanogaster
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P-PSDB; ABB69630.
                                                                             ABL13733 standard;
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0312, PR0290, PR0341, PR0535, PR0619, PR0317, PR0809, PR0810, PR0818, PR09105, PR01005, PR01005, PR01005, PR01005, PR01011, PR01131, PR01133, PR01182, PR01184, PR01187, PR01281, PR0319, PR0319, PR03194, PR03117, PR01110, PR02094, PR03115, OR PR021981, PR0 antagonists can be used to inhibit tumour cell growth. The PR0 polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other
                                                         717 CCCGTGCGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGG
                                                                           777 AGAGAAACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGT
                                                                                                                                                       diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithalial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thirty PRO polynucleotides encoding PRO polypeptides, useful in treatment, diagnosis and prevention of cancer
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                                                                                                                                                                                                                                       877
                                                                                                                                                                                                               837 AGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO2145 núcleotide sequence SEQ ID NO:76.
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                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                AAC58395 standard; cDNA; 1509
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99WO-US12252.
99US-0141037.
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99WO-US28313.
99WO-US30911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 50; Fig 57; 286pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe CK,
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20-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1355 TCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAAT 1414
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                                                                                                                                                                                                                                                                This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster.
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                                                                                                                                                                           New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 411.4; DB 21; Length 2886;
Pred. No. 1.3e-104;
); Mismatches 256; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 other;
                                                                             Schulte T;
                                                                                                                                                                                                                                   Claim la; Page 8-12; 26pp; German.
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68.88;
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                                                                             Adamczewski M, Oellers
                                                                                                                 2000-014207/02.
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nes 565; Conserv
                                                                                                                                     P-PSDB; AAY50814
                                         (FARB ) BAYER
   04-MAY-1998;
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93 GGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAG 152
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anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, and sugiogenic and immunologic disorders. AAC58242 to AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAB24089 represent human the property of the complication of the human property.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 AGGCTGGTCCTTGGATCTGCAGATGCAGA------GGCAGATATCAGTGGCTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGC
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                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                              Score 377.2; DB 21; Length 1509;
Pred. No. 3.6e-95;
                                                                                                                                                                                                                                                                                                                Pred. No. 3.6e-95;
0; Mismatches 633; Indels
                                                                                                                                                                                                                                                               Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                                                                                                                                                                                                                                  25.1%;
55.2%;
                                                                                                                                                                                                                                                                                                                               811; Conservative
                                                                                                                                                                                                                                    present invention.
                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                 1113 GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCC
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                                                                                                                                                                                                                                  1053 GATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAG
                                                                                                                                                                                                                                                                                                                                                        1173 TCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                 1233 CACGGATTTCCGTCGGTCGTTCGTCCGTCCGTCCACGATGGAAGACGTGGGCGCGGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              1231 GCCTGCTCCCCCACGCACGATGAGCACCTCCTGCACGGTGGGCAACCCCCCGAGGGGG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTGATAGGTTTTGCCTGTTCGTGTTCACACTTTTCACAATCATCGCGGACAGTAGCTGT
GCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCC
                                                                                 873 ATTGATAGCCCAGTACTTCGCCAGCACCATGATCATCGTGGGCCTCTCGGTGGTGGTGAC
                                                                                                                  933 TGTGGTGGTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGAT
                                                                                                                                                                           993 AAAATCAGTATTCCTACAATGGTTGCCATGGATACTGCGAATGTCGAGGCCAGGGAAGAA
                                                                                                                                                                                                                                                                1053 CAAGGTGCGCCCGGCCTGCCAGCACAAGCAGCGGCGCTGCAGCCTGGCCAGTGTGGAGAT
                                                                                                                                                                                                                                                                                                                          1113 GAGCGCCGTGGCGCCGCCGCCCGCCAGCAACGGGAACCTGTACATCGGCTTTCCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1353 GATGAAGAAGGCTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGCTGCGATGGT
                  CCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCTGTGTACTGAC
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5-hydroxytryptamine; 5-HT3; calcium ion conductance;
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ligand-gated receptor; ds.
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                                                                                                                                                                                                                    The present sequence is the coding sequence for wild-type human alpha7 natochica ecetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
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                                                                                                       Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
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Pred. No. 2.9e-94;
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                             MΒ;
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                                             GTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATAAGAAGACGAACCTT
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                                                                                                                                                                                                                                                                                                                               A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian ocytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs.
                                                                                                                                                                                                                                                      Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 374; DB 18; Length 1
Pred. No. 3.2e-94;
0; Mismatches 635; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
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                                                                                                                                                                                                                                                                                                  Disclosure; Page 71-73; 108pp; English.
                                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES
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55.1%;
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809; Conservative
                                                                                                                                                                               Harpold MM
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P-PSDB; AAW09025.
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This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (naChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 naChR activity or cytoprotective agents, e.g. antisense compounds activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 naChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (incline) and response to these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171
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                 cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
            Alpha? nAChR; alpha? nicotinic acetylcholine receptor subunit; canc neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetyl-choline receptor sub-unit - used to identify modulators of
the receptor, potentially useful for treating neuro-degeneration,
cancer, affective disorders etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 1590;
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                                                                                                                                                                                                                                                                                                                                                                         Monteggia LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding variant of human alpha7 nicotinic
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Pred. No. 3.8
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al Similarity 55.1%;
808; Conservative
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                         292 CAGGGGTGAAGACTGTTCGTTTCCCAGATGGCCAGATTTGGAAACCAGACATTCTTCTCT
                                                 ATAATAGTGCTGACGAGGCTTTTGACGGGACCTACCAGACCAACGTGGTGGTCAGAAGCG
                                                            395 GCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACATCG
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Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunits or specific receptor provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction and design of more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                     TTGATAGGTTTTGCCTGTTCGTGTTCACACTTTTCACAATCATCGCGACAGTAGCTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                             Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "neuronal nicotinic acetylcholine receptor alpha-7 subunit"
                                                                                                                                                                                                                                                                                                                                          ; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; tissue; screening; NAChR; antibody; ds.
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                                                                                                                                   1475 TGTTATCGGCACCGCATATCATCGTG 1500
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Length 1876;
  DB 15;
          Pred. No. 4.1e-94;
  Score 373.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elliott
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immunochemistry;
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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are subustantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in present sequence represents a human neuronal NAChR alpha7 subunit
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Pred. No. 4.1e-94;
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide.
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coding sequence

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Human; alpha7 nicotinic acetylcholine gated ion chann
5-hydroxytryptamine; 5-HT3; calcium ion conductance;
         human alpha7 ligand gated ion channel
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                                                                                                                                                                                       The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline
Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
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Pred. No. 8e-94
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RESULT 13 AAC90385 (first entry)

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AAC90385

RESULT 14

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5-hydroxytryptamine; 5-HT3; calcium ion conductance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Special cell culture medium for treating cells and for inducing mammallan cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline residue and the wild-type cysteine residue at position 241 substituted by a serine residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAG
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                                                                   Human; alpha7 nicotinic acetylcholine gated ion channel; mutant; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Pred. No. 2.3e-93;
0; Mismatches 637; Indels 24;
alpha7 ligand gated ion channel coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 other;
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qa	162 CTTCTCCCTGAGCCTCCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAACCAC 221	
٥y	213 CAATATATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGGAACGACGACGAGGAGTA 272	
QQ	CAAATGTCT	
oy .	73 TGGCGGGGTCAAGACTCAGGATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTAT 33	
g	82 TCCAGGGGTGAAGACTGTTCGTTTCCCAGATGGCCAGATTTGGAAACCAGACATTCTTCT 34	
Oy Dp	333 GTATRATAGTGGTGACGAGGGTTTTGACGGCACCTACCAGACCAGGCGGGGGGGG	
Qy	393 CGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACAT 452	
qa		
Oy.	453 CGCGTGGTTTCCCTTCGACGACCAACACTGTGAAGTTCGGTAGCTGGACATATGA 512	
qa	462 ACGCTGGTTTCCCTTTGATGTGCACACTGCAAACTGTGGTTTGGGTCCTGGTCTTACGG 521	
Qy	3 CGCAATCAGTTGGATCTGGTGCTAAAAGATGAGGCAGCGGCGATCTATCGGACTTCAT 57	
đ	522 AGGCTGGTCCTTGGATCTGCAGATGCAGGAGGCAGATATCAGTGGCTATAT 572	
& E	573 AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGG 632 [	
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g q		
ò	693 GTACTACTTCTTCAACCTGATCGTCCCGTGCGTGATCTCATCGATGGCACTCCTCGG 752	
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οg	753 GTTCCTGCTTCCTGCAGATTCCGGGAGAAGATTCCCTGGGGATAACAGTCTTACTCTC 812	
٥y	813 GCTGACGGTGTTCCTCAACCTGGTAGCCGAGGACCCTGCCACAGGTCTCCGACGCTATCCC 872	
QQ	ATGCTGCTCGTGGCTGAGATCA	
ķ é	873 CCTGTTAGGGACGTACTTCAATTGCATCGTCATGTAGCGTCGTCGTGGTGGTACTGAC 932	
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0y	3 AAAATCAGTATTCCTACAATGGTTGCCATGGATA	
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Dp	1053 CAAGGTGCGCCCGGCCTGCCAGCAAGCAGCGGCGGCGTGCCTGGCCAGTGTGGAGAT 1112	
Οÿ	1113 GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATGATGATGATGATGACGACGGCCC 1172	
qa	1113 dagcgccgrdgcgccgccgccagcaacggaaccrgcrgracarcggcrrccgcg 1172	
Qy	1173 TCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCG 1232	
qa	CCCGACTCTGGGGTAGTGTGGCCGCAT-	
Qy		
qq	1231 GCCTGCTCCCCCACGCACGATGAGCACCTCCTGCACGCGGGGAACCCCCCGAGGGGG 1288	

Search completed: August 21, 2003, 04:24:43 Job time : 409.032 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 21, 2003, 00:04:15; search time 5602.3 Seconds (without alignments) 10975.350 Million cell updates/sec US-09-303-232-5\_COPY\_95\_1597 1503 1 atggcccctatgttggcggc......caccgcatatcatcgtgcaa 1503 5777422 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gaport 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb\_ba:\* gb\_htg:\* gb\_in:\* gb\_om:\* gb\_ov:\* GenEmbl:\* Database :

em\_htgo\_hum:\* em\_vi:\* em\_htg\_hum:\* em\_htg\_inv:\* em\_htg\_mus:\* em\_htg\_pln:\* gb\_vi:\* em\_ba:\* em\_fun:\* gb\_ro:\* gb\_sts:\* gb\_sy:\* em\_pl:\* em\_ro:\* em\_sts:\* em\_ov:\* em\_pat:\* em\_in:\* em\_mu:\* еш\_un:\* em\_or:\* gb\_pat: \*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Description	0047 11014 04144		E58348 Nucleic aci	AF321447 Drosophil	AF321445 Drosophil	AJ554209 Drosophil	AF321448 Drosophil	AF3Z1449 DFOSOPNII AF143846 Heliothis	AX009612 Sequence	E58347 Nucleic aci	AJSS4ZIU Drosophil	AY036613 Drosophil	AX009610 Sequence	ESB346 NUCLEIC act	Y08420 H.sapiens m	AF385585 Homo sapi	040583 Human alpha x43604 B taurus mR	L31619 Rattus ratt	S53987 nicotinic r	X/U29/ H.sapiens m L25827 Human a7 ni	AX054567 Sequence	AR282833 Sequence	AA/19068 Sequence U62436 Human nicot	AF225980 Mus muscu	AR261850 Sequence	BD023656 Variant n AR055255 Sequence	AR071403 Sequence	AR173187 Sequence	ARZZ4030 Sequence AX054575 Sequence	AX054577 Sequence	L37663 Mus musculu	AXUS45/9 Sequence	X68586 G.qallus mR	Chicken a	247962 Danio r	RTS		bp mRNA linear INV 27-MAY-1999 nicotinic acetylcholine receptor alpha		WOrm)	a. Ottorogota	Artnropoda; Hexapoda; Insecta; Frerygota; ota; Lepidoptera; Glossata; Ditrysia;	OCHINGO, MOLLOCHIO. Adamovekski M
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OY 541 GATGAGCCAGCGATCTATCGACTTCATAACAAATGGGGAGTGGTATCTAATAGGA 600	601 ATGCCAGGCAAAAAGAACACAATAACATACGGTGCTGCCCCGAGCCCTACGTGGACGTC 66	Qy 661 ACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATGGTCG 720	QY 721 TGCGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGCTCCGGAGAG 780	QY 781 AAACTCACACTTGGAGTCACTATTCTTCTATGGTGAGGGTGTTCCTCAACCTGGTAGCC 840	QY 841 GAGACCTGCCACAGGTCTCCGACGCTATCCCCTGTTAGGGACGTACTTCAATTGCATC 900	Oy 901 AIGHTCATGGFACGTCTCTGGFACTGACTGTGGTGGTGCTACTCAATTACCACCATCGA 960	OY 961 ACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCA 1020	Qy 1021 TGGATACTGCGAATGTCGAGGCCAGGGAAGATCACCAGGAAGACTATAATGATGAC 1080	Qy 1081 ACGAGGATGAGGGAGCTGGAACTGAAGGTGGTCGAGGTCCTTGCTGGCGAATGTT 1140	OY 1141 CTAGATATTGATGATGACTTCAGACCCCTCCGCCTCCTAACAGTACTGCCTCGACC 1200	Qy 1201 GGGAATTTGGGACCTGGGTGCTCAATATTCCGCACGGATTCCGTCGGTCG	Oy 1261 CCGTCCACGATGGAAGACGTGGGCGGCTGGTTGGGTAGCCACCATCGCGAGCTGCACCTC 1320	QY 1321 ATACTGAGAGCTGCAGTTCATCACGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAG 1380	Oy 1381 CTGATCAGCGACTGGAAGTTTGCTGCGATGGTTGTGATAGGTTTTGCCTGTTCTTGTTC 1440	QY 1441 ACACTTTCACAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGT 1500  1535 ACACTTTTCACAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGTG 1594	Oy 1501 CAA 1503 Db 1595 CAA 1597	RESULT 2 AX009614 LOCUS AX009614 3109 bp DNA linear PAT 06-SEP-2000
TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits	JOURNAL Unpublished  REFERENCE 2 (bases 1 to 3029)  AUTHORS Schulte,T., Oellers,N. and Adamczewski,M.  TITLE Direct Submission JOURNAL Submitted (19-APR-1999) ZF-HTB. Baver AG. Bldg. O 18. Leverkusen	51368, Germany Location/Qualifiers ce 1. 3029	/mol_type="mRNA" /db_xref="taxon:7102" CDS 95 .1600	/note="Nyacanta/-2" /coon_start=1 /product="putative nicotinic acetylcholine receptor alpha /-2 subunit"	/procent_la="Analyse99.1" /db_xref="G1:4895007" /translation="MAPMLAALALLALLPVSEQGPHEKRLINALLANYNTLERPVANE /translation="MAPMLAALALLALLPVSEQGPHEKRLINALLANYNTLERPVANE STEPLEVREGITLQOI IDVDEKNOLLITINIALSLEWNDYNIARMDSSTGGVGDIRTTPN STEWNDSTRUK	CDMKFGSWTYDGNOLDLVLKDEAGGOLGDFTUGEWYLIGWCKWTTTYACCPEPYV DVTFTIMIRRRTLYYFRILIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFL NIABTLEPOVSDALPLELGYYFROLTOWEWYNSKSVLIGHEMPONIKSV NIABTLEPOVSDALPLELGYYFROLTOWEWYSSWALLGFTLPPDSGEKLTLGVTILLSLTVFL FOUT DAGTI PROPECKYTPOKTTENTANWTREAFFTLTWFHRTRAFHTREAFFTSF	PENNING THE TENNING TO THE TRANSPORT TO	Ouery Match 100.0%; Score 1503; DB 3; Length 3029; Best Local Similarity 100.0%; Pred. No. 0; Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaos 0;	1 ATGCCCCTATGTTGCCGCCTTGCCGCCTTTGCTGCCTGTTGCTGCAAGGT 60 HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	61 CCTCACGAGAAGAGCCCTGCTTGCTGCGAACTACACACCCTGGACGACCGC 1  11111111111111111111111111111111	121 GTGGCCAACGAGAGCGAACGCTAGAGGTCAGGTTGGCTTGACCTTGCAGCAAATCAT 18 11	181 GACGTGGACGAGAGAATAACTACTTATAACCAATATGGCTGTCGTTGGAGTGGAAT 24  181 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	241 GACTACAACCTGAGGTGGAACGACGAGTATGGCGGGGTCAAGGACCTCAGGATCACG	301 CCCAACAAGTTGTGGAAGCCGGACGTCTTATGTATAATAGTGCTGACGAGGTTTTGAC 305 CCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGACGAGGTTTTTGAC 305 CCCAACAAGTTGGGAAGCCGGACGTCCTTATGATATAATAGTAGTAGAAGGCGAAGGCGAAGACCGTAATAATAATAATAGTAGAAGAGTTTTGAAGAAGACCGAAGACCTTATAATAATAATAGTAGAAGAGTTTTTAATAATAATAAT	361 GGGACCTACCAGACCAACGTGGTGGTCAGAAGCGGGGCAGTTGCCTGTACGTGCCACCT 41511111111111111111111111111111111111	GGCATATTCAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCACAC 48	Qy 481 FGFGATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAA 540 

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KLWKPDVLMYNSADGETDGTVOTNVVNSGGSCLYVPPGIFKSTCKMDIAMFPEDOH
CDMKFOSWYDGNOLDLVLKGEAGGBLSDFITNGEWYLIGMPGKKNTITYACCEBTY
DVFFTIMIRRTLYFFNLIYPFTNLISSMALLGFTLPPDSGERLTLGVTILLSLTVFL
NLVAFTLEOVSDAIPLIGFYFNCINFWVSGSVVLTVVVLYHHRTADIHEMPOMIKSY
FLOWLWHITRASRFOKKITRKTIMMYRMRELELEKERSSKSLLANVLDIDDDFRHGFH
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
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tive 0; Mismatches
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/db_xref="G1:9996847"
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DFRHTISGSQTAIGSSASFGERPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD 
EAELIGDWKFRAMVURFCLLVFTLFTIIATVTVLLLSRHIIVQ**
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                                                                                                                                                                                                                Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type III (nAcRalpha-30D) mRNA, complete cds, abra114.7
                                                                                                                                                                                                                                                                                                                                                                                      Chases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ine substitution;
in GenBank Accession
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
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Pred. No. 1.1e-193;
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Drosophila melanogaster
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379. .1863
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/dev_stage="embryo"
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LSIITVELNIVAETLEQVSDALPLIGTYFNCIMFWASSVVLITVVLIWYHHRTADIHEM
PHYKSVFLQMLPWILMRREDGRKITRYTILLSNRWRELELKERSSKSLLANVLDIDD
PFRHTISGSQTALGSASFGRPTTVEEHHTAGCNIKDLHLILKELQFITARWRKADD
EAELIGDWKFAAMVVDRFCLIVFILFIIATVTVLLSAPHIIVQ"
                                                                      /translation="MOSPLPASLSLEVLLIFLATIKESCOGPHEKRLLNHLLSTYNTL
ERPVANESEPLEVKFGLTLQQIIDVDEKNQILFTNAWLNLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITW
/product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                                                  FPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
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                                                                                                                                                                                                                                                                                                                                                                                /note="results in isoleucine to methionine substitution; compared to variant clone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG
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                                                                                                                                                                                                                                                                                     /note="results in asparagine to glycine substitution; compared to variant clone" /replace="gg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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compared to variant clone"
/replace="9"
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/note="compared to variant clone"
/replace="a"
1560
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/replace="t"
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Pred. No. 1.4e-188;
); Mismatches 405;
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llarity 70.1%;
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-1 Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                     1490 AGGAGCTGGAGCTAAAAGGAGCGCTCCTCCAAATCCCTGCTGGCCAATGTCCTCGACATGT 1549
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                                                                              1151 ATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGG 1210
                                                                                                                                                                                                                                                        1628 TGGAGGAGCATCACACGCCCATCGCAATCACAAAGATCTTCATCTAATTCTCAAAG 1687
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//gene="nAcRalpha-30D"
/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a and
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     GGGAGCTGGAACTGAAGGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTG
                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford 30x, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
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/organism="Drosophila melanogaster"
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Drosophila melanogaster
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/db_xref="taxon:7227"
/chromosome="2"
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Grauso, M. and Sattelle, D.B.
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	/note="results in glycine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" Yeplace="aa"	pha-30D" s in glycine to asparagine substitution;	EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ" 793794	FFRITIGS FLUGHLF FLUGHGRFORM I LULSHAMPELLER BENSANSHALLAN ULLUN DER FRITIGS GOOT ALGES ASSESTED FROM THE FLUGH FL	CCPEPYVDITFIJOIRRRTLYYFRULIVPCYLISSMALLGFTLPPDSGEKKITLGYTL LSLIVPLNLVAESMPTTSDAVDLIGTFROLIMWASSYVLTVVVLNYHRTADIHEM PPPLIKSVFLOWLPPILEMORPGRKITRKTILLSNNMKELELKERSSKSLLANVLDIDD	DEAL I FUNDAMARD UM NOSABEGEDOLI INTRA VARIBGOSOLI VEPOLEASI CAMBILIA FPPDDQHCEMFEGNITYDGNQLDIVLINGSDGDLEDFINGEMYLLAMPGKRITI VA TODBDAVIDT MEM TAT BORDI VA PENIT TUDAVI TOSMI TOMIT	/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL ERPVANESEPELEVKECHTLQDIIVDEKVQLLITNUKLLEWNDYNIRWIEFEKGKY TO ETTENKY ERPDII ERPOINT WERE REGEROME URBEITUNG GOT VURGET ERFERENTERE	/protein_id="AAM13593.1" /db_xref="GI:20152847"	/product="nicotinic acetylcholine receptor Dalpha6 subunit variant type II"  "Acceptor id="nauloog";"	exolls 3D	eurotransmitter transmembrane	יים אלים אלים אלים אלים אלים	"Ovrde	on:7227" 2"	osophila melanogaster" NA"	iflers	Oxford, South	.U.B. N Himan Anatomy and Genetics-Punctional		e-mRNA Editing -1533 (2002)	ed Target of Adenosine Deaminase Acting on		Culetto R and Sattelle.D R	Lilopoda, Hexapoda, insecta; a, Diptera, Brachycera, Muscomorpha; idae, Draschila	- 1			(nAcRalpha-30D) mRNA, comple	2023 bp mRNA linear INV 29-APR-2002			CARTCATCACCACACACTOTCCTOTCTCCCCCACCACCACCACCACCACCACCACCACCACCAC			
TOTGGAAGCCGGAACCTCGTAATCTATAATAATGGTCGAAGGGTTTGGAGGGCTTTGCAAGCCGGGAACCCGAACCTAGCCAACCTGGCATACCTAGCGAACCAACC	/note="results in gly compared to the seque Number AE003626" /replace="aa" variation 794	/gene="nAcRalpha-30D" /note="results in gly	,	DEFRICE	CCPEEYVDITETIC LSLTVFLALVAESH PPWIKSVFLOWLDW	FPFDDQHCEMFGG	/translation=' ERPVANESEPLEVR	/protein_id="# /db_xref="GI:2	/product="nicc variant type 1	/codoustart-1	/yene= incratpina-5		/map="30b1" //dev stage="em	/db_xref="taxc /chromosome="2	/organism="Drc /mol_type="mRN	rce		Grauso, M. Direct Sub	2 (bases		New and Highly Conserve			Bunalyola, metazoa, ni Neoptera, Endopteryota Enhydroidea, Drogonhili	NISM	AF321446.1	NO		2	RESULT 6 AF321446	000	1401	7 7	1748	
	AGCTGCAGTTCATCACGCCCAGGATGAAGGCTGATGAGGAAGCCGAGCTGATCAGCG	TGGAGGAGCATCACGGCCATCGGCTGCAATCACAAGATCTTCATCTAATTCTCAAAG	TGGAAGACGTGGGCGGCGGCTGGGTAGCCACCATCGCGAGCTGCACCTCATACTGAGAG	C   C   C   C   C   C   C   C   C   C	GACCTGGGTGCTCGGTCGGGATTCCGTCGGTCGTTCTCCGTCCG	なられるとは、これでは、これでは、これでは、これでは、これでは、これでは、これでは、これで	ATGATGACTTCAGACACGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGG   I			ではなってものであることであることであるのでは、ないでもでもできないとなっておしまして、または、これをおしてもできましています。		GAATGTCGAGGCAGGGAAGATCACCAGGAAGATTATAATGAAAAAAAA	TACATGAAATGCCACAGAGATAAAATCAGTATTCCTACAATGGTTGCCATACATA	TCGCCTCGTCGTGGTGCTGACAGTAGTGGTGCTCAACTACCACCATCGCACAGCGGACA	TAGCGTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCACCATCGAACAGCTGATA	CCCAAGTATCTGATGCAATCCCCTTGTTAGGCACCTACTTCAATTGCATCATGTCATGG	この日本の中田の日本で日本のの日田本本の日田の本田のであるのでは、日本の日田の日の日の日の日の日の日の日の日の日の日の日の日の日の日の日の日の日の	**************************************			TACAAATTCGTCGCCGTACATTATATTTTTTTTTTAATTCGTGCCATGTGTGTAA	TCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCGTGCGTG		AAAAGAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCA	GAGGGGATCTTTCCGATTTCATAACAAATGGCGAGTGCTTGCT	51 GCGGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCA	90 AATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGATTTGGTTTTGAATTCCCGAAGATG	91 AGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGATGAGGCAG	AGAGCACATGCAAGATAGACATCACGTGGTTCCCATTTGATGACCAACATTGCAAATGA	AGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCACACACTGTGATATGA	ACACCAACATTGTGGTCAAACATAACGGCAGTTGTCTGTACGTGCCCCCTGGTATCTTCA	AGACCAACGTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCA		TGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC	

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AJ554209 GI:29466434
AACRALPha-30D gene; nicotinic acetylcholine receptor subunit Dalpha6.
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                                                      791 TTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGC
                                                                                                     CACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGG
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases I to 1665)
Direct Submission
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/note="results in glycine to serine substitution; compared to variant clone" /replace="a"
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                                                             /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626 and in variant clone"
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    AATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGATTTGGTTTTGAGTTCCGAAGATG
                                                                                                                                                                                         TCTCATCGATGGCACTCCTCGGCTTCACACTGCCACAGACTCCGGAGAGAAACTCACAC
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                                                                                                                                                                                               /protein_id="Cad86935.1"
/db_xref="G1:29466435"
/td_xref="G1:29466435"
/td_nslation="MDSPLPASLSIPVLIFIAIIKESCOGPHEKRLINHLLSTYNTL
ERPVARESEPLEWYEGTLILQQIIDVDEKNQLLITNIMLSLEWNDYNLRWEFEYGGYV
ERPVARESEPLEWYEKTGOTYLDYDEKNQLLITNIMLSLEWNDYNLRWEFEYGGYV
ERPVARESEPLEWYEKTGOTYLDYDSENGGELSPETNGEWYLLAMPGKNUTTVY
CCPEPYVDITFFIIGNERPLYYFENLIYPCVLISSMALLGFTLPPDSGEKITTVYA
CCPEPYVDITFFIIGNERPLYFEYETNILYPCVLISSMALLGFTLPPDSGEKITTVYA
CLSITYFLNIVARENMPTRINYFEYTLILRWARELERERSSGELLANTLDID
PPWIKSVFLQMLPWILMGRORKITTRYTILLSWARELERERSSGSLLANTLDID
ERALIGDWAFRAAMVUDFCLIVFTLETIIATVTVLLSAPHIIUQ"
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Department of Pharmacology, eet, London, WCIE 6BT, UNITED
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                                                                                                                                                             /codon_start=1
/product="nicotinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                          /gene="nAcRalpha-30D"
/product="nicotinic acetylcholine receptor
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 Submitted (31-MAR-2003) Millar N.S., Department o
University College London, Gower Street, London,
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.8e-188;
es 407;
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Pred. No. 9.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    400
                                                                /organism="Drosophila
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                /gene="nAcRalpha-30D"
                                                                                                                       /gene="nAcRalpha-30D"
                                                                                                                                                /gene="nAcRalpha-30D"
                                        Location/Qualifiers
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ilarity 69.9%;
Conservative 0
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Best Local Simi
Matches 1044;
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AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG 130
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 /note="compared to the sequence deposited in GenBank
Accession Number AE003626"
                                                                                          GenBank
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Accession Number AE003626"
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                                                                                          /note="compared to the sequence deposited
Accession Number AEO03626"
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Pred. No. 4.8e-179;
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Best Local Similarity
Matches 1058; Conserv
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                                                                                                                                                             Grauso,M., Reenang,R.,, Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6, and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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VLWTHRFADIHEMPPMIKSVFLQMLPWILMGRPGRLTFRCTILLSNRMKELELKE
VSKSLLANVLDIDDPRHTISGSGASTGFRTTVEEHHTAICCNHKDLHLIL
KELQFITARMRKADDEAELIGDWKFAAMVVDRPCLIVFTLFTITATVTVLLSAFHIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDSPLPASLSLFVLLIFLAIIKESCOGPHEKRLLNHLLSTYNTL
ERPVANESEPLEVKFGLTLQQIIDVDEKNQILTTNAMLNLDEKNQLLITNLWLSLEWN
DYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKRSGSCLYV
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/note="results in methionine to isoleucine substitution;
compared to the sequence deposited in Genbank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                            Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford Ox1
30x, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="results in arginine to histidine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
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                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a,
8b; contains two repeats of the functional domain lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="nicotinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="nAcRalpha-30D"
/note="results in serine
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Number AE003626"
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/protein_id="AAM13395.1"
/db_xref="G1:20152851"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="embryo"
1. .2068
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                  GI:20152850
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1359
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CCPEPYUDITFTIQIRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVFLALVAESMPTTSDAVPLIGYTILLSLTVFLNLVAETLPQVSDAIPLLGTYFN
LSLTWRYASSVVLTVVVLNYHRRTADIHEMPPNIKSVFLQWLPWILRNGRPGRKITRKT
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TAIGCNHKDLHIIKELQFITARMRKADDEAELIGDWKFAAMVVDRFCLIVFTLFTII
ATVTVLLSAPHIIVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"nicotinic acetylcholine receptor Dalpha6 subunit
variant type V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDSPLPA$LSLFVLLIFLATIKESCOGPHEKRLLNHLLSTYNTL
ERPVANESEPLEVKFGLTLQ011DVDEKNQILTTNAMLNLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKMDITW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 8a an
8b; contains two repeats of the transmembrane TM2 region"
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/notew"results in methionine to isoleucine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                   Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OXI
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                            /db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                              /dev_stage="embryo"
                                                                                                                                                                                     Location/Qualifiers
                       11973307
2 (bases 1 to 2110)
Grauso, M. and Sattelle, D.B.
Direct Submission
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Rovel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-Mediated A-to-I Pre-mRNA Editing

AL Genetics 160 (4), 1519-1533 (2002)
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1369
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                                                                                                                                                         866 CTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCTGTGG
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AGAGCGAACCGCTAGAGGTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACG			TGGGCGTAACTATACTATCATTAACAGTATTTCTAAACCTTGTGCCGAGTCCATGC   TGGGCGTAACTATCATTAACAGTATTTCTTATTCTTCTATCGCTGACGTGT 	
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3629 bp mRNA linear INV 27-MAY-1999
Heliothis virescens putative nicotinic acetylcholine receptor alpha
7-1 subunit mRNA, complete cds.
AF143846
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1 (bases 1 to 3629)
Schulte, T., Oellers, N. and Adamczewski, M. Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
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YNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDF
GGVKDLRVPPRHLMKPDVLMYNSADBEGEDSTYFTNVVVRNNGSCLYYPPGIFKSTKI
DITWFPFDDQRCEMKFGSYTYDGYQLDLQLQDBGGGDISFYTNGEWELIGVPGKRNE
IYYNCCPEPYIDITANVIRRKTLYYPFNLIYPCVLLASMALLGFTLPPDSGEKLSLG
VTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFWVASSVVSTILILNYHRRAD
THEMSDWIRCVFLYWLPWVLRNSRPGSATTPPPARVPPPDLELRENSSKSLLANVLD
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                                                                                        184 ACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCGCACGGATTTCC 1243
                                                                                                                                                                                1244 GTCGGTCGTTCGTCCGTCCGTCCACGATGGAAGACGTGGGCGGCGGCGGGCTGGGTAGCCACC 1303
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Schulte, T., Oellers, N. and Adamczewski, M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. O 18,, Leverkusen
                                                                                                                                                                                                                                                                                                                                                             1364 CTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGCTGCGATGGTTGTTGATAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1424 TTTGCCTGTTCGTGTTCACACTTTTCACAATCATCGCGGACAGTAGCTGTTGTTGTG

    3629
    /organism="Heliothis virescens"
/mol_type="mRNA"

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/db_xref="G1:4895005"
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/note="hvnachra7-1"
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/LTABES 14 101 = "MOGRARRSHLAAPAAGLLLLCLLWPRGARCGYHEKRLLHHLLDH
YNVLRRPVWRSDPLQLSFGLTLMQTIDVDBKNQLLTNTHKLLENNDMNLRWNTSDF
GGVKDLRVPPRLWRPDVLWNSADBGFDSTYPTNVVRNNGSCLYVPPGTFKSTCKI
DITWPFPDDQRCEMREGSWTYDGSYQLDLQLQDBGGGDISSFYTNGBMELIGYPGKRNE
IYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLG
THLLGSLYFNAMAFENPATSDAPULGYFYRCTIMPWASSYVSTTLIAVHHRAD
THEMSDWIRCYFLWLPWVLBMSRPGSATTPPPARVPPDFDLELRRESSKSLLANVLI
IDDDFRHPQAQQPQCCRYYRGGEBNGAGLAAHSCFGVDYELSLIKFIRYTTDQMRKD
 ATACTECGAATGTCGAGGCCAGGGAAGAACACACGAAGAAGACTATAATGATGAACACG -1083
                                                                                                                                                                                                                                                ------GTGTCGACTACGAGCTCTCCCTCATT 1642
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                                                                      CGGCGCCGGACCTGGAGCTGCGGAGCGCTCCAAGTCGCTCCTAGCGAACGTGCTC
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Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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953 c 944 g 910 t
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Nucleic acids encoding acetylcholin-receptor subunits
Patent: EP 0962528-A 3 08-DEC-1999;
BAYER AG (DE)
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/note="unnamed protein product"
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/protein_id="CAC07500.1"
/db_xref="G1:9996845"
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931 c 922 g 895 t 1 others
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1211 ACGATGCCAGCGACGTCGGACGTGCCCTTGCTCGGCACCTACTTCAACTGCATCAGT 1270
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Pred. No. 1.1e-141;
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PAT 06-SEP-2000

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Nucleic acid encoding insect actyl choline receptor subunit.
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1448 CCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCTC
                            GATATTGATGATGACTTCAGACACGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGG
                                           1561 ATACTACAGGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCACAGTTGCTTCG----
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JP 2000023680-A/2.
Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Lepidoptera; Glossata; Dirrysia;
Noctuoidae; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3701)
Martin,A., Nadja,E. and Thomas,S.
Mucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 2 25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUEUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, A01K67/033, C07K14/7/05, C07K16/28, C12N1/21, C12N5/10,
C12Q1/68,
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0; Mismatches 460; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:7102"
953 c 944 g 910 t
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Location/Qualifiers
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JP 2000023680-A/2
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NSSERGGYNFDLAIPPHELWKPDVLAYNSABGESTDGTYATNVVRNNGSCLYVPROFIK
STCK IDITWPFPDDQRCEMKRGSWTYDGFQLDLQLQDBGAGDISSTINGEWDLLGVP
GKRNEIYYNCCPEPYIDITFALLIRRYTLYYFPNLIVECVLIASMALLGFTLPBDSGE
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HRNDDTHEMSEWIRVIFLYWLDCILLEWQRPGQVGYECPPPPSSSSSASGEKKQQIQN
VEKERSKSKSLANVLDIDDDFRCNHRCASATLPHQPTYRPWYRQGDDGSVGPVGPA
GPVVDGRLHEAISHFCLTSSAEYELALILKELRWITEQLKKEDETSDITRDWKFAAMV
VDRLCLIIFTLFTIIATLAVLFSAPHFIVSGVRG"
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Street, London, WCIE 6BT, UNITED
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                                                    TCCACGATGGAAGACGTGGGCGGCGGGTAGCCACCATCGCGAGCTGCACCTCATA
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Drosophila melanogaster
Brusryota: Metazoa, Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila
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Submitted (31-MAR-2003) Millar N.
University College London, Gower
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26. .1654
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                                                                                                   TACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCC
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1532 AAATTTGCTGCCATGGTCGTCGATGTTTGCTGCTTATATTTTCACCTTGTTTACTATT 1591
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1 (bases 1 to 2907)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify in Naw and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                   1412 TCCCACACCTGTCTGACATCCTCTGCGGGGTACGAACTGGCGCGCTGATACTCAAGGAGCTG
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AGACCCGGACAGGTTGGCTACGAATGTCCGCCGCCGCCTCTTCTTCGAGTTCCTCCGCA
                           1066 ACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGGAGGTCGTCGAAGTCC
                                        1126 TTGCTGGCGAATGTTCTAGATATTGATGACTTCAGACACGGCCCTCCGCCTCCTAAC
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Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FG
University of Oxford, South Park Road, Oxford Oxl 3Qx, UK
Location/Qualifiers
1. 2907
/Organism="Drosophila melanogaster"
/Mol.Type="mRNA"
/db_xref="taxon:7227"
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Drosophila melanogaster
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/gene="nAcRalpha-34E"
/allele="A"
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Grauso, M. and Sattelle, D.B.
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Pred. No. 4.5e-131;
0; Mismatches 540;
Similarity 61.0%;
12; Conservative
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tion tion tion tion tion tion tion tion	2892712 /gene="nAckalpha-34E" /note="ion channel; neurotransmitter transmembrane receptor netrotinic acetylcholine receptor Dalpha5 subunit. /broduct="nicotinic acetylcholine receptor Dalpha5 subunit. /db_xref="di:20152840" /translation="waradakutrebubbELWLAVRLAHCSSNFSSSSTRTTSSNORH /translation="waradakutrebubbELWLAVRLAHCSSNFSSSSSTRTTSSNORH /translation="waradakutrebubbELWLAVRLAHCSSNFSSSSSTRTTSSNORH /translation="waradakutrebubbendergebaschestergebarderge	oha-34E"  d to B allele"  ha-34E"  in phenylalanine to isoleucine  compared to B allele"  in threonine to isoleucine substitu  allele"  in lysine to argenine substitution;  allele"	Treplace" gg "  Yegne="results in deletion of asparagine and serin compared to B allele"  Treplace""  Mote="results in serine, glycine, and asparagine insertion: compared to B allele"  Yepne="nAcRalpha-34E"  Mote="results in serine, glycine, and asparagine insertion: compared to B allele"  Yepne="nAcRalpha-34E"  Agene="nAcRalpha-34E"  Agene="nAcRalpha-34E"  Anote="results in asparagine to serine substitutio compared to B allele"  Treplace="esults in asparagine to serine substitutio compared to B allele"  Treplace="gentle allele"  Treplace="gentle allele"  Treplace="gentle allele"	34.7%; Score 521.6; DB 3; Length 2907; Conservative 0; Mismatches 519; Indels 51; Gaps 4; GTCCTCACGAGAGGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCG 116

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NMLSPKTAAAATAAGDEATTQQPTNIRL/CARKRQRLRRRRKRKPATPNETDIKKQQQL
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                                                                                                                             GAGAGGAGCTGCAGTTCATCACGGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGAT 1385
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
AGACGTGGGCGGGCTGGGTAGCCA-----CCATCGCGAGCTGCACCTCATACT
                                                                                                                                                                                                      CAGCGACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT
                                                                                      TGCGGTCACCCATCATACGTGCATCAAATCAACTGAATATGAATTAGGTTTAAATCTT
                                                                                                                                                      2532 AAAGGAAATTCGCTTTATAACTGATCAGCTACGTAAAGATGACGAGTGCAATGACATTGC
                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2834)
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foote="non channel; neurotransmitter transmembrane
receptor: exon 5 is excluded due to exon skipping,
generates a loss of reading frame and a truncated
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1 3QX, UK
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Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetion
University of Oxford, South Parks Road, Oxford OX1 3QX,
Location/Qualifiers
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Drosophila melanogaster
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/organism="Drosophila
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SMPPFKTRKSTDTYSTPAAITSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
VLQVLLVSLQQWQLHYQQRSVLLFRRIAASTIAFISYLGSFAAQLRSSSSSSNSSNS
GNSSSYQILOGLNKHSWIFLLIYLNISAKVCLAGYHEKRLHDLLDPYNTLERPVLNE
SDPLQLSFGLTLMQIIDVDERNQLLYNVWHKLEWNDMNLRWHTSDYGGVKDLRIPPH
RIWKPDVLMYNSABGFBGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
CEMKFGSWTYDGFQVCPANVTRSITTAARNPI"
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1016 2098	1065 2158	1106	1166 2278	1215 2338	1274 2398	1325 2458	1385 2518	1445 2578
TCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTT 	GCCATGGATACTGCGAGTGTCGAGGCAGGAAGATCACCGGGAAG	1066	1107 GGAGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGATGACTTCAGACA	1167 CGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCT 2279 CAATTGTCGCCCCATGACGCCCGGGGAAACACTGCCACACACA	1216 GGGTGCTCAATATTCCG-CACGGATTTCCGTCGGTCGTTCGTCCGTCCGTCCACGATGGA	1275 AGACGTGGGCGGGCTGGGTAGCCA	1326 GAGAGAGCTGCAGTTCATCACGGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGAT 	1386 CAGGGACTGGAAGTTTGCTGCATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT
957	1017	1066	1107	1167 2279	1216 2339	1275 2399	1326	1386 2519 1446 2579
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:
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(without alignments)
2698.100 Million cell updates/sec
Perfect score: 2665
Sequence:
1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

830525

830525 seqs, 258052604 residues

Searched:

Database: SPTREMBL\_23:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_tung1:\*
4: sp\_human.\*
5: sp\_invertebrate:\*
6: sp\_nammal:\*
7: sp\_mhc:\*
10: sp\_phage:\*
10: sp\_phage:\*
11: sp\_rodent:\*
12: sp\_vrius:\*
13: sp\_vretebrate:\*
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	Description	O9xzi3 heliothis v	08t7v5 drosophila	Q9vwi9 drosophila	Q9xzi4 heliothis v	Q8t7s2 drosophila	Q8t7s1 drosophila	Q8t7s3 drosophila	Q8t7s0 drosophila	Q8t7r9 drosophila	Q9v179 drosophila	Q8ipe2 drosophila	Q9vjt9 drosophila	Q9jhd6 mus musculu	003481 gallus gall	P91197 caenorhabdi	Q81932 caenorhabdi
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## ALIGNMENTS

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T.1  99XZI3 PRELIMINARY; PRT; 496 AA.  99XZI3;  90XZI3;  90 Careabed;  90 - NOV-1999 (TrEMBLrel. 12, Last sequence update)  101-NOV-1999 (TrEMBLrel. 23, Last annoctation update)  101-NAR-2003 (TrEMBLrel. 23, Last annoctation update)  101-NAR-2003 (TrEMBLrel. 23, Last annoctation update)  101-NAR-2003 (TrEMBLrel. 23, Last annoctation update)  102 Last Careabed (Noctuid moth) (Owlet moth)  103 Noctuidae; Heliothinae; Heliothis receptor alpha 7-1 subunit.  104 Noctuidae; Heliothinae; Heliothis.  105 Noctuidae; Heliothinae; Heliothis.  106 Noctuidae; Heliothinae; Heliothis.  107 Noctuidae; Heliothinae; Heliothis.  108 SEQUENCE FROM N.A.  108 Schulter T., Oellers N., Adamczewski M.;  108 Schulter T., Oellers N., Adamczewski M.;  109 Schulter T., Oellers N., Adamczewski M.;  100 Schulter T., Oellers N., Adamczewski M.;  101 Schulter T., Oellers N., Adamczewski M.;  101 Schulter T., Oellers N., Adamczewski M.;  102 Schulter T., Oellers N., Adamczewski M.;  103 Schulter T., Oellers N., Adamczewski M.;  104 Schulter T., Oellers N., Adamczewski M.;  105 Schulter T., Oellers N., Adamczewski M.;  106 Schulter T., Oellers N., Adamczewski M.;  107 Schulter T., Oellers N., Adamczewski M.;  108 Schulter T., Oellers N., Adamcz	Gaps
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T.1  O9XZ13  PRELIMINARY; PRT; 496 AA.  O9XZ13  O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)  O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)  O1-NOV-1999 (TrEMBLrel. 23, Last annotation update)  D1-NOV-1999 (TrEMBLrel. 23, Last annotation update)  D1-NOV-1999 (TrEMBLrel. 23, Last annotation update)  Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;  Neopters: Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuo Noctuidae; Hellothinae; Hellothis.  Neopters: Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuo Noctuidae; Hellothinae; Hellothis.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SCHULT T. Oellers N., Adamczewski M.;  SCHULT T. O	Score 2665; DB 5; Length 496; Pred. No. 1.3e-244; 0; Mismatches 0; Indels 0
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RA Admanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendelle J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                   Length
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                     C8B4F6B34287C8C8 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                 DB 5;
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                                                                                        LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV
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MEDLINE-21969411; PubMed-11973307;

MEDLINE-21969411; PubMed-11973307;

Grauso M., Reaena R.A., Culetto E., Sattelle D.B.;

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Genetics 160:1519-1533(2002).

-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-1 - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL; AF272778; AAM13390.1; -

-1 - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878.
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
Ffam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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                                                                          31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-Marive nicotinic acetylcholine receptor alpha 7-2 subunit.
1-Mellothis virescens (Noctuid moth) (Owlet moth).
1-Mearyota, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota, Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                          Gaps
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Schulte T., Oellers N., Adamczewski M.;
Schulte T., Oellers N., Adamczewski M.;
Futtative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF143847; AAD32698.1;
                                        45;
     Length
                                        Indels
                                        36;
   76.8%; Score 2046.5; DB 5 77.7%; Pred. No. 9.4e-186;
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                                      32; Mismatches
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Interpro; IPR006202; Neur_chan_LBD.
Interpro; IPR006029; Neu_channel_memb
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Pfam; PF02932; Neur_chan_memb; 1
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGRO0860; LIC; 1.
Query Match
Best Local Similarity 77.7%.
Matches 394; Conservative
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Neur\_channel

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SEQUENCE 49
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                                                                                                                                                                                              STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
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                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21969411; PubMed-11973307; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-T Pre-mRNA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELLONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321446; AAM13393.1; -.
Flybase; FB9n0032151; nAcR-alpha-30D.
                                                                              27;
                                                         501;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, wetazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                    score 1803.5; DB 5; Length
Pred. No. 1.1e-162;
                                                                              Indels
                                 56704 MW; 43CB0DC3960C78AB CRC64;
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1. Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                              78;
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                                                      67.7%; Score 1803.5;
68.7%; Pred. No. 1.1e
                                                                              Mismatches
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                                                                              53;
                                                                             Matches 347; Conservative
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                                  501 AA;
                                                                  Similarity
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SEQUENCE FROM N.A.
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                       Transmembrane
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                                  SEQUENCE
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Q8T7S2;
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MEDLINE=21969411; PubMed=11973307;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                          494;
                                                                                                                             PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Ephydroidea; Drosophilidae; Drosophila
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23, Last annotation update)
                                                                                                                                                                                                                                     ; Score 1795.5; DB 5;
; Pred. No. 6.1e-162;
54; Mismatches 81;
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PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                    Neur_chan_LBD.
Neu_channel_memb
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Drosophila melanogaster (Fruit fly)
                                    InterPro; IPR006029; Neu channel_I
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                              56048 MW;
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68.18;
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IPR006201;
IPR006202;
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New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533(2002).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY:
EMBL; AF321447; AAM13394.1; -
Flybase; FBgn0032151; nAcR-alpha-30D.
                                                                                                                                                                                                                                   Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type INACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                           494;
                                                                                                                                                               Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                           Length
                                                                                                                                                                                                         k; Score 1792.5; DB 5; Length
b; Pred. No. 1.2e-161;
55; Mismatches 81; Indels
                                                                                                                                                                                     494 AA; 56113 MW; 48327537229573FF CRC64;
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                                                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                               Interpro; IPR006201; Neur_channel.
Interpro; IPR006202; Neur_chan_LBD.
Interpro; IPR006029; Neu_channel_memb.
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                                                                                                                Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                          67.3%;
67.9%;
                                                                                                                                                                                                                                341; Conservative
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                                                                                                                                                                          Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21969411; PubMed-11973307; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha5, and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGFDSTYPTNVVVRNNGSCLYVPPG1FKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 PARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
                                                                                                                                                                                                            IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 AA; 56095 MW; B46EBEDA63A92942 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 1790.5; DB 5 67.9%; Pred. No. 1.8e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Mismatches
                                                                                                                                                                                                                                                                                                            InterPro; IPRO06202; Neur_chan_LBD.
InterPro; IRRO06029; Neur_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                               EMBL; AF321445; AAM13392.1; --
FlyBase; FBgn0032151; nAcR-alpha-30D.
InterPro; IPR006201; Neur_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0860; LIC;
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                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1774; DB 5;
Pred. No. 7.1e-160;
4; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02932; Neur_chan_memb; 1.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0032151; nAcR-alpha-30D. InterPro; IPR006201; Neur_channel. InterPro; IPR006202; Neur_channel_memb. InterPro; IPR006029; Neu_channel_memb.
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Pfam; PF02932; Neur_chan_memb; 1
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=7227;
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Best Local Simil
Matches 341; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 TILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRHPQAQQPQCCRYYRGGEENGAGLAA------HSCFGVDY-ELSLILKEIRVIT
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                    01-JUN-2002 (TrEMBLE). 21, Last sequence update)
01-MR-2003 (TrEMBLE). 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 AA; 59110 MW; 1C200AF74F87F841 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1769; DB 5;
Pred. No. 2.2e-159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRRAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
523
                                    Created)
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 64.4
Matches 342; Conservative
 PRELIMINARY;
                                      (TrEMBLrel.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane
                                    01-JUN-2002
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445

RESULT Q8T7R9

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RATAIN-BEACKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashbunner M., Hedderson S.N.,

RA Gocay R.A., Lewis S.E., Richards S., Ashbunner M., Hedderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Channe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beson K.Y., Bencs P.V., Barenda B.P., Bhandari D., Bolshakov S.,

RA Berson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Dahlke C., Perraz C., Ferriard S., Pleischmann W.,

RA Bartin D., Houston K.A., Dangan-Rocha S., Dunkov B.C., Dunn P.,

RA Bortin D., Houston K.A., Garg N.S., Gelbart W.M., Glasser K.,

RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Hartis M.,

RA Hartis N.L., Mayus P., Heiman T.J., Well M.-H., Theeyam C.,

RA Hartis N.L., Mayus P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Hartis N.L., Mayus W., Murphy B., Liu X., Mattei B., McIntosh T.C., Morris J., Woshrefi A.,

RA Hartis N.L., May W., Murphy B., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Hartis N.L., May W., Murphy B., Nuson K., Stroel K., Welsen B.,

Ra Blazzolo M. Pittama G.S., Pan S., Pollard J., Wang X.,

Ra Blazzolo M. Pittama G.S., Pan S., Pollard J., Wang X.,

Ra Shue B.C., Siden-Klamos I., Simpson M., Strong R., Wassenbach J.,

Ra Harts R., Tector C., Turner R., Venter E., Wang A.,

Mulliams S.M., Woodage T., Stapson M., Strong R., Wassenbach J.,

Ra Jener X., Pong E.W., Mollo G.W., Weissenbach J.,

Ra Jener S., Rober E., Shon H., Worley S., Chaeler F., Shen H.,

Ra Jener S., Rober E., Shon S., Rollo G., Wun D., Yang S., Zhu X., Smith H.O.,

Ra Jener S. Ra, Pace B., Woll Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galler R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., MOY M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Petel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., CG4128 protein.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. Created) Last sequence update) Last annotation update) 554 PRT; 13, 22, 01-MAR-2003 (TrEMBLrel. 23, Science 287:2185-2195(2000) PRELIMINARY; (TrEMBLrel. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=7227; 01-MAY-2000 01-OCT-2002 RESULT 10 **09VL79** g 

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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLQLQDEGGGDISSFVTNGEWELIGV-PGK------RNEIYYNCCPEPYIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YYRGGEENGAGLAA-----HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 117; Gaps
                                                                                SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell I Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.W.J., Smith E., Shu S., Swutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

"Annotation of Drosophila melanogaster genome.";
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 554;
                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003626; AAF52817.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02932; Neur_chan_memb; 1.
PRINTS: PR00252; NRIONCHANNEL.
TIGREAMS: TIGRO0860; LIC; 1.
PROSITE; P00236; NEUROTR_LON_CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.7%; Score 1484.5; DB 5 Best Local Similarity 53.6%; Pred. No. 2.7e-132; Matches 310; Conservative 53; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KLSLG--
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InterPro; IPR006029; Neu_channel_memb.
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    RAMEDLINE-20196006; PubMed-10731132;
RAMBIA M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RAMBIA M.D., Celniker S.E., Li P.W., Hiskins R.A., Galle R.F., Goorge R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., Sutton G.G., Mortman J.R., Yangol Q., Chen. L.X., Randon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Nan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L., Ram Abril J.F., Agbayoni A., An H.J., Madrews-Pfannkon C.R., Gabor G.L., Ram Abril J.F., Agbayoni A., An H.J., Baraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Barnedle J., Bayraktaroglu L., Beasley E.M., Benckova D., Botcham M.R., Bouck J., Brokstein P., Botchiarkov S., Berkova D., Botcham M.R., Bouck J., Brokstein P., Botchiarkov S., Burkova D., Botcher A., Deng Z., Mays A.D., Dow I., Dietz S.M., Aborkova D., Botcher A., Dang Z., Mays R.D., Dow I., Dietz S.M., Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Acherry J.M., Cawley S., Dunkow B.C., Dunn P., Robstein M. J., Evangelista C.C., Ferraz C., Ferraz C., Ferrac C., Gabrielian A.E., Garg N.S., Glan P., Harris M., Alush F., Karpen G.H., Gu Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattei B., McIntosh T.G., Morris J. Mosherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D., Nelson D.L., Melson D.R., Natue B.E., McIntosh T., Strong M., Strong K., Sinch T., Shu B., McIntosh K., Nasskern D.R., Pacled J.M., Shu B., Spier E., Spradling A.C., Staplecon M., Strong K., Sinch T., Shu B., Williams S.M., Woodager, Worley K., Wun D., Yang S., Yao Q.A., Ye J., Walshe R., Tector C., Turner R., Venter E., Wang K., Williams S.M., Woodager, Worley K., Zhon W., Strong R., Shu B., Williams S.M., Woodager, Worley K., Zhon W., Zhung S., Zhan M., Zhong W., Zhung S., Zhan M., Zhang W., Zhu Wang S., Wang Sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S. E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Bancon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Petel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Last sequence update)
Last annotation update)
                                                                                                                       525 AA
                                                                                                                                                         Created)
                                                                                                                       PRT;
                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:2185-2195(2000).
                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                        NACRALPHA-30D.
                                                                                                                                      Q81PE2;
01-MAR-2003
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QBIPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 -----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 -----ATSDAVPLLGTYFUNWVAETMP-----ATSDAVPLLGTYFNCIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFT
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                                                                                                                                                                 Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M., J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Annotation of Drosophila melanogaster genome.";
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1371; DB 5; Length 525;
Pred. No. 1.6e-121;
6; Mismatches 108; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003626; AAN10709.1; -
SEQUENCE 525 AA; 60135, MW; CF95283C56EA90A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.4%; Scc
Best Local Similarity 52.2%; Pre
Matches 290; Conservative 56;
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                                                                                     Submitted (MAR-2000)
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DO GOVING TEMBELLE: 13. Lested D.

DO GOVING TEMBELLE: 13. Lested D.

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DO GOVING TEMBELLE: 15. Last Sequence update)

DO GOVING TEMBELLE: 15. Last Sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 FNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 GVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 LQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 ARVPPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                Campbell K.
th C.D.,
            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emrmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 156;
                                                                                                                                                                                                      Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 273;
                                                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003642; AAF53374.2; -.
HSSP; P58154; 119B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 48.0%; Score 1279; DB 5;
Best Local Similarity 57.6%; Pred. No. 3.7e-113;
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0028875; nAcR-alpha-34E
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006201; Neur_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247; Conservative
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SEQUENCE FROM N.A.
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01-OCT-2000
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                                                                                                                                                                                                                                                                              FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ENGAGLAAHSCFGV------DYELSLILKEIRVITDQMRKDDEDADISR 458
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                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                          EDKVRPACQHKP------RRCSLASV-ELSAGAGPPSSNGNLLYIGFRGLEGMHCA
                                                                                                                                                                                                                                                                                                                                                                                              1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                        Gaps
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                     Stitzel J.A., Farnham D.A., Collins A.C.,
"Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain.";
                                                                                                                                                                                                                                                                                      PRINTS; PR00252; NRIONCHANNEL.
TIGRERMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NBURORT ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                       502 AA; 56617 MW; C9353E5136D620E3 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Nicotinic acetylcholine receptor subunit alpha.7.
                                                                                                                                                                                                                                                                                                                                                        46.6%; Score 1242; DB 11;
47.1%; Pred. No. 2.7e-109;
ative 90; Mismatches 139;
                                                                                                                                            Brain Res. Mol. Brain Res. 43:30-40(1996)
                                                                        SEQUENCE FROM N.A.
STRAIN-DBA/21bg;
MEDLINE-97189245;
PARTINE-97189245;
                                                                                                                                                                                                                                                                                                                                                                            Matches 243; Conservative
                             musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                               SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10090;
                                                                                                                                                                        STRAIN-DBA/21bg;
                                                                                                                                                                                  Stitzel J.A.;
                                                                                                                                                                                                                                                                                                                             Transmembrane
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73 VDEKNQVLITNAWLQMYWVDIYLSWDQYEYPGVQNLRFPSDQIWVPDILLINSADERFDA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TFHTNVLVNYSGSCQXIPPGILKSTCYIDVRWFPFDVQKCDLKFGSWTHSGWLIDLQMLE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 FMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 VDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 TYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQD
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                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 21, Last sequence update)
Alpha8 subunit of nicotinic acetylcholine receptor precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superiments:

**Substitution 1:35-48(1990).

**I- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

**I- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

**I- SIMILARITY: BELDONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

InterPro: IPRO06201; Neur_channel.

InterPro: IPRO06202; Neur_channel_memb.

Pfam; PF02931; Neur_chan_LBD.

Pfam; PF02931; Neur_chan_LBD; 1.

Pfam; PF02932; Neur_chan_memb; 1.

PRIGRAMS; TIGNO0860; LIC; 1.

PROSITE; PS00236; NEUROTR_ION_CHANNEL: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90315158; PubMed-2369519; Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 1219.5; DB 13; Lengt
46.3%; Pred. No. 3.9e-107;
iive 88; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10F362D153EC87A7 CRC64;
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511 AA
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                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 46.3
236; Conservative
                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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  459 1
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                                                        459
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                                                                                                                                                                                                                       003481;
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                                                                                                                                     RESULT 14
Q03481
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72 72 132

249

418

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7;
419 AGLAAHSC-FGVDYE-----LSLILKEIRVITDQMRKDDEDADISRDWKFAA 464
                                                                                                                              : | | | | : | : | | | 414 SKSGKITCPLSEDNEHVQKKALMDTIPVIVKILEEVQFIAMRFRKQDEGEEICSEWKFAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 EKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
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al Similarity 46.2%; Score 1141; DB 5; Length 46
al Similarity 46.2%; Pred. No. 9.8e-100;
218; Conservative 85; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Gattung S., Maggi L.;
"The sequence of C. elegans cosmid D2092.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6182A7F827357B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.7 kDa protein.
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Hypothetical protein; Glycoprotein; Ionic channel;
Postsynaptic membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA
                                                                                                                                                                                                                                             465 MVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U88167; AAB42223.1;
WormPep; D2092.3; CE09102.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_channel.memb.
Ffam; PP02931; Neur_chan_LBD; 1.
Ffam; PF02932; Neur_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
370 PK----HHPSLKNTEMNVL--
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SEQUENCE 461 AA; 52718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches 21
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                152 GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG----DISSFVTNGEW
                                                          208 ELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPP
                                                                                                                 268 DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILN
                                                                                                                                                                                                                                     388 ANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLIL-----KEIRV
                                                                                                                                                                                                                                                                                                             494
                                                                                                                                                                                                                                                                                              443 ITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM
                                                                                                                                                                                                      326 LHFRSADSHEMNPLVRRVLLEFLPWLLFMSRPG----
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# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 13, 2003, 15:14:55; Search time 10.386 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-4 2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Description	P22770 gallus gall	4 homo s	~			P48180 caenorhabdi	P91766 manduca sex				P09480 gallus gall	P09478 drosophila	P12389 rattus norv	Q07263 bos taurus	PO4757 rattus norv							-			rattu		P18845 carassius a	P12390 rattus norv	P02709 bos taurus	P43143 rattus norv	P25162 drosophila	10	PO4756 mus musculu
SUMMARIES	ID	ACH7_CHICK	ACH7_HUMAN	ACH7_MOUSE	ACH7_RAT	ACH7_BOVIN	ACH1_CAEEL	ACH1_MANSE	ACH1_SCHGR	ACH3_HUMAN	ACH2_HUMAN	ACH2_CHICK	ACH1_DROME	ACH2_RAT	ACH3_BOVIN	ACH3_RAT	ACH2_DROME	ACHA_CHICK	ACH6_HUMAN	ACH3_CHICK	ACHN_CHICK	ACHA_TORMA	ACH4_CHICK	ACHP_HUMAN	ACHN_HUMAN	ACHP_RAT	ACHA_TORCA	ACH3_CARAU	ACHN_RAT	ACHA_BOVIN	ACH6_RAT	ACH4_DROME	ACHA_RAT	ACHA_MOUSE
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	Query Match Length	502	502	502	502	499	498	516	557	503	529	528	267	511	495	499	576	456	464	496	491	461	622	498	502	495	461	512	200	457	493	519	457	457
æ	Query Match	47.5	46.8	46.6	46.2	45.7	45.1	36.8	36.7	36.0	36.0	36.0	35.9	35.7	35.1	34.9	34.7	34.5	34.4	34.4	4	34.0	33.9	ω,	33.9	33.8	33.7	ъ.	ω,	33.6	ω.		33.4	33.4
	Score	1267	1246	1241	1232.5	1218.5	1201	980.5	979	096	096	959	956.5	951	936.5	930	926	918.5	918	917	908.5	906	904	903.5	902.5	905	899	898.5	868	896.5	896.5	893.5	890	883
	Result No.	1	7	m	4	S	9	7	ω	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	. 58	53	30	31	32	33

P26153 gallus gall P49581 gallus gall	P19370 carassius a Q98880 brachydanio	P05377 xenopus lae P04755 drosophila	P45963 caenorhabdi P09483 rattus norv P02708 homo sapien	
ACHP_CHICK ACH6 CHICK	ACHA_CARAU ACHA_BRARE	ACH2_XENLA ACH3_DROME	ACH8_CAEEL ACH4_RAT ACHA_HIMAN	ACH5_RAT ACH0_HUMAN
~ ~				
470	459	457	538 630 482	452
33.3	33.0	32.9	32.7	32.2
888 886.5	885.5 880 879.5	876.5 874	872 867.5 866.5	858.5 855.5
34 35	36	98 4	4 4 4 1 2 2 2	44

### ALIGNMENTS

RESULT 1 ACH7_CH1CA AC
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LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120

61

MGLRALMLWLLAAAGLV-----RESLQGEFQRKLYKELLKNYNPLERPVANDSQPLT

12.1 LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT

181 YDGYQLDLQLQDEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK

360

404

---IDDDFRHPQAQQ

241 İLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 300

301 VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG 404 GVICGRMTCSPTEEENLLHSGHPSEG-DPDLAKILEEVRYIANRFRDQDEEEAICNEWKF 462

463 AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494 

463

POCCRYYRGG - - EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF

E-----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS 403

361 SATTPPPARVPPPDLELRERSSKSLLANVLD----

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN
'Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPPIC TECTUM BETWEEN E5 AND B16.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                      FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                         "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; Nature 359:500-505(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L->S,T: SUPPRESSES INHIBITION BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1267; DB 1; Length 502;
; Pred. No. 6.8e-100;
83; Mismatches 144; Indels 36;
                                                              CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC
                                                                                                                                                                                                                                      SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPEN-CHANNEL BLOCKER QX-222
QR -> ET (IN REF. 3).
                                                           MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO MEDLINE-93024917; Pubmed-1383829; Galzi J.-L. Devillers Thiery A., Hussy N., Bertrand S. Changeux J.-P., Bertrand D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ransmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHA-7 CHAIN.
EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
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Best Local Similarity 48.65
Matches 249; Conservative
                nicotinic receptor.";
Nature 353:846-849(1991).
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PDB; 1KL8; 17-APR-02.
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502 AA;
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Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
"Human alpha 7 acevylcholine receptor: cloning of the alpha 7 subunit
from the SH-SY5Y cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97062879; PubMed-8906617; MEDLINE-97062879; PubMed-8906617; Ellist S.B. Berckhan K.J., Urrutia A., Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits ", 1:217-228(1996).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
              P36544; 015826; 096RH2; 099555; 09BXH0; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1997 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuronal acetylcholine receptor protein, alpha-7 chain precursor. CHRNA7 OR NACHRA7.
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502 AA
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MEDLINE-94195283; PubMed-8145738;
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                                                                                                                                                                                                                                                                                                                                                                         expressed in Xenopus oocytes
  STANDARD;
                                                                                                                                       Homo sapiens (Human).
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[4]

MEDLINE=97162233; PubMed=9009220; Groot Kormelink P.J., Luyten W.H.M.L.;

Groot Kormelink P.J., Luyten W.H.M.L.;

"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";

FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helnemann S.F.; "Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riley B., Williamson M., Collier D., Wilkie H., Makoff A.; "A 3-wb map of a large segmental duplication overlapping the alpha7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14."; Genomics 79:197-209(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: MW-54157.68; METHOD-MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
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                                                                                                                                                                                                                                                                                                                                        TISSUE-Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orug Dev. Res. 30:252-256(1993)
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Genomics 19:379-381(1994).
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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EMBL; X70297; CAA49778.1;

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                                                                                                                                                                                MIM; 118511; -

R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
R GO; GO:0004899; F:nicotinic acetylcholine-activated cation-se. .; TAS.
R GO; GO:000087; P:activation of MAPK; TAS.
R GO; GO:0006832; P:small molecule transport; TAS.
R InterPro; IPR006029; Neu_channel_memb.
R InterPro; IPR006029; Neu_channel_memb.
R InterPro; IPR006020; Neu_channel_memb.
R Pfam; PF02931; Neur_channel.
R Pfam; PF02931; Neur_chan_LBD; 1.
R Pfam; PF02931; Neur_chan_memb; 1.
R Pfam; PF02932; Neur_chan_memb; 1.
R PRINTS; PR00252; NRIONCHANNEL.
R TIGRPAMS; TIGR00860; LIC; 1.
R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R PASSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R PASSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R TABSSE MEMBRANER; 1010, C channel; Glycoprotein; Signal; TANSSE MULtigene family.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

A -> G (IN REF. 1 AND 7).

S -> N (IN REF. 2 AND 6).

C -> S (IN REF. 8).

A -> G (IN REF. 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSOCIATED WITH RECEPTOR ACTIVATION
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D94B3A482EAA0E42 CRC64;
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BY SIMILARITY.
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                                  EMBL; L25827; -; NOT_ANNOTATED_CDS.
EMBL; 223141; CAA80672.1:
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               U62436; AAB40114.1; -.
Y08420; CAA69697.1; -.
AF385585; AAK68111.1;
                                                                                         EMBL; AF33758; AAK19515.1;
PIR; GO2259; GO2259.
PIR; 137185; ACHUA?
Genew; HGNC:1960; CHRNA7.
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U40583; AAA83561.1;
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Matches 240; Conservative
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502 AA;
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DISULFID
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                                                                    392
                                                                                                                   416
                                                                                                                                                               452
                                                                                                                                                                                                                452
-----VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                            QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                               393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylcholine receptor.";
Genomics 26:399-402(1995).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE-Brain; MEDLINE-9534936; PubMed-7601470; Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.; "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                            DADISRDWKFAAMVVDRLCLIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                    SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006029; Neu_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD: 1.
Pfam; PF02932; Neur_chan_LBD: 1.
PRINTS; PR00252; NRIONHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                    -----SATTPPPAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L37663; AAC42053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00860; LIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                -DEHLLH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                         ACH7_MOUSE
P49582;
                                                                                                                                                                                                                                                            453
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TRANSMEM
                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                                                                          LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
                                                                                                                                                                                                                                                                                                                                                                                           LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT 180
                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                             YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDKVRPACOHKP-----RRCSLASV-ELSAGAGPPTSNGNLLYIGFRGLEGMHCA
                                                                                                                                                                                                                                                          1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ENGAGLAAHSCFGV-----DYELSLILKEIRVITDQMRKDDEDADISR
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93147931; PubMed-7678857;
Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
"Molecular cloning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
                                                                        ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                             44;
                                                                                                                                                                                             Length 502;
                                                                                                                                                                                                         pred. No. 1.1e-97;
90; Mismatches 139; Indels
                                                                                                                                                             C9312E5226D120E3 CRC64;
                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||| |||||||| : |:|||| |: :||||| : :
EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                             DB 1;
                                                                                                                                                                                             Score 1241; DB 1;
Pred. No. 1.1e-97;
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                                               POTENTIAL.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                             56631 MW;
                                                                                                                                                                                             46.68;
                                                                                                                                                                                                                             243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
280
317
469
490
164
213
                                                                                                              46
                                                                                                                           90
133 1
502 AA;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
262
296
318
470
150
212
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                                                              DISULFID
                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                           113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH7_RAT
Q05941;
                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                               CARBOHYD
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                               Query Match
Best Local
 TRANSMEM
               TRANSMEM
                                               FRANSMEM
                                 DOMAIN
                                                                                                                                                                                                                               Matches
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Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Long;
                                                                                                                                                                                                                                                                                                                                               ACH7_BOVIN
P54131;
                                                                                                                                                                                                                                                 399
                                                                                                                                                                                                                                                                                                                                                                                                            CHRNA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                LITTED (AUG-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                           SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                     SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 5.8e-97;
83; Mismatches 141; Indels
                                                             Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P -> F (IN REF. 2)
P -> R (IN REF. 2).
00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%; Score 1232.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                EMBL; L31619; AAC33136.1; -...
PTR; 701378; T01378.
InterPro; IPR0066029; Neu_channel_memb.
InterPro; IPR0066029; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Ffam; PP02931; Neur_chan_LBD.
Pfam; PP02931; Neur_chan_memb; 1.
Prints; PR00352; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                             STRAIN-Sprague-Dawley; TISSUE-Brain;
                                           STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Multigene family SIGNAL 1 22 BY
          Neurosci. 13:596-604(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 P
                                                                                                                                                                                                                                                                                                                       EMBL; S53987; AAB25224.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.28;
                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR00860; LIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230
255
280
280
317
469
490
164
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90
133
447
469
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
262
262
296
318
470
150
                                                                                   REVISION TO 363
                                                                                                        Hartley M.;
Submitted (
 calcium.";
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS;
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122 MYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 PQAQQPQCCRYYRGGEENGAGL--AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADIS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPDSGVVCGRLACSPTHDEHLMHGAHPSDG-DPDLAKILEEVRYIANRNRCQDESEVIC 457
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                                                                                                                                                                                                                                                                                                                                                                                                                          PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 ATTPPPARVPP-------PPDLELRERSSKSLLANVLDIDDDFR-----H
                                                                                                                                                                          242 LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
                                                                                                                                                                                                                                                                                                                      DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine chromaffin cells: molecular cloning, functional expression and allernative splicing of the alpha 7 subunit.";

Eur. J. Neurosci. 7:647-655(1995).

-:-FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=P54131-2; Sequence=VSP_000075; TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adrenal meduila;
MEDLINE-95346009; PubMed-7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQQCKLKFGSWSYGGWSLDLQMQE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 VLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFASTM 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGARC------GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID 72
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                                                                                                                                               359 RRCSLASVEMSAVAGPPATNGNLLYIGFRGLDTMHCAPTPD-----SGVVCGRVACSP
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (in isoform Short).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 1218.5; DB 1; Length
46.1%; Pred. No. 8.9e-96;
Live 80; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                  EMBL; X93604; CAA63802.1; -...
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=269194778;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0860; LIC; 1.
PROSTIE; PS00236; NEUROTR_LON_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLCHOLINE RECEPTOR LIKE
               449 ESBAVCSEWKFAACVVDRLCLMAFSVFTILCTIGILMSAPNFV 491
452 EDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
POTENTIAL.
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                                                                                                         498 AA
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PIR, S68588; S68588.
HSSP, P58154; I198.
WormPep; F2566.3; CE09639.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006201; Neur_channel_
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS: PR00252; NRIONOHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 258:261-269(1996).
[2]
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                                                                                                         STANDARD;
                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                                       ACH1_CAEEL
P48180;
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                                                                                                                                                                                                                                                                                                                    372
                                                                                                                                                                      NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG 196
                                                                                                                                                                                                                                                                     SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316
                                                                                                                                                                                                                                                                                                                                                                                                                               -----NRHSESLIRNIKDNEHSLSRANSFDADCRLNQYIMTQSVSNGLTSLGSIPSTM 417
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                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                245 LMTLLGFTLPPDAGEKITLQITVLLSICFFLSIVSEMSPPTSEAVPLLGIFFTCCMIVVT
                                                                                                                                     LLISCAILAAPTLGSLQERRLYEDLMRNYNNLERPVANHSEPVTVHLKVALQQIIDVDEK
                                                                                                                       NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT
                                                                                                                                                                                                                     DISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA
                                                                                                                                                                                                                                                                                                                    SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGS----ATTPPPARVPP
                                                                       17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                   PPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC-CRYYRGGEENGAGLAA-----
                                                  Gaps
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J. NEUROSCI. 10:879-889(1998).

FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98424077; PubMed=9753155;
Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
Eaytham H.M., Lind R.J., Wolnarcht S.;
Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
"Characterization of a nicotinic acetylcholine receptor from the insect Manduca sexta.";
Eur. J. Neurosci. 10:879-889(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                 30;
                                                89; Mismatches 151; Indels
                          Length
 E463ABB40AC9FA82 CRC64;
                        45.1%; Score 1201; DB 1; 46.0%; Pred. No. 2.7e-94;
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FTIFIIVSTIGIEWSAPYLV 497
57169 MW;
                                                Conservative
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                                   al Similarity
230; Conservat
498 AA;
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P91766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQDEGGG----
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                                                                                                                                                                                                                                                                                                1.
channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                   ACETYLCHOLINE RECEPTOR PROTEIN, ALPHALIKE CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.8%; Score 980.5; DB 1; Length 516; 40.5%; Pred. No. 1.5e-75; tive 75; Mismatches 159; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
BY SIMILARITY
                                                                                                                                 EMBL; Y09795; CAA70928.1; -.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; IOnic changes.
                                                                                                or send an email to license@isb-sib.ch)
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40.58; FAU
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nes 205; Conserv
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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PRINTS; PR00252; NRIONGHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROPF, ION.CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1 CHAIN.
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                                                                                                                                                                                                MEDLINE-91092263; PubMed-1702381;
Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
Darlison M.G., Sattelle D.B., Barnard E.A.;
"Sequence and functional expression of a single alpha subunit of an
                                                                                                                                                                                                                                                                         FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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                                                                                                               Schistocerca gregaria (Desert locust).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
NCBL_TaxID=7010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.7%; Score 979; DB 1; Length 557; 40.0%; Pred. No. 2.2e-75; ive 88; Mismatches 160; Indels
                                                                       01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-Ll chain precursor.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                       557 AA
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
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Pfam; PF02932; Neur_chan_memb: 1
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Matches 217; Conserv
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                             01-NOV-1991 (Rel.
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243 YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP 302
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                                                                                                                         63
                                                                      71 IDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| ||||||| |: :::| | || ||||||:| ::||| |:| ::| ||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
      11 AAPAGLLLLCCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding for the alpha 3 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACH3_HUMAN STANDARD; PRT; 503 AA.

92297; 015823; 096RH3; 099553; 09B093;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update).
01-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR NACHRA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-90245296; PubMed-2336208;
Fornasari D., Chini B., Tarroni P., Clementi F.;
"Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 AQQPQCCRY----YRGGEENGAGLAAH------SCFGVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-97062879; PubMed-8906617;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mihovilovic M., Roses A.D.; "Expression of mRNAs in human thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a neuronal acetylcholine receptor.
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Thymus;
MEDLINE=91114756; PubMed=1989896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurosci. Lett. 111:351-356(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
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Strausberg R.L., Felungul 124/7513.

Ribitaberg R.L., Felungul 124/7513.

Ribitaberg R.L., Felungul 124/7513.

Ribitaberg R.L., Felungul 124/7513.

Ribitaberg R.L., Felungul E.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Boitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheeter T. E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Withing M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G., Whiting M., Madan J.W., Green E.D., Dickson M.C., Anders R.W., Green E.D., Dickson M.C., Anders A.C., Shevohenko Y., Bouffard G.G., Butterfield Y. S.N., Krzywinski M.I.J., Skalska U., Smailus D.E., Schnerch A., Schein J.S., Mors S.J.M., Marra M.A., Thuman and mouse chuk services "J. Marra M.A.,"

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-97162233; PubMed-9009220;
Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven mAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";
FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                   Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNA3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.; "Characterization of the human beta4 nAChR gene and polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M., "Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21342809; PubMed=11450844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                             MEDLINE=99118870; PubMed=9921897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum. Genet. 46:362-366(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Epidermal keratinocytes;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 30-503 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 6-493 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHRNA3 and CHRNB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE.
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Event-Alternative splicing; Named isoforms=2;

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Many, 118303; C:nicotinic acetylcholine-gated receptor-chan...; TAS.
RGO; GO:0005892; C:nicotinic acetylcholine-activated cation-se...; TAS.
RGO; GO:0005812; F:transporter activity; TAS.
RGO; GO:000165; P:signal transduction; TAS.
RGO; GO:0006832; P:signal transduction; TAS.
RGO; GO:0006832; P:signal transduction; TAS.
RGO; GO:0006832; P:signal transduction; TAS.
RITERPRO; IPR006202; Neur_channel_memb.
RITERPRO; IPR006202; Neur_channel.
RP Ffam; PF02931; Neur_channel.
RP Ffam; PF02932; Neur_channel.
RP RASTE; PF000522; NRIONCHANNEL.
RRCPETO; IRROWGEO; LIC; I.
RRCPETO; PS01236; NEUROTR ION CHANNEL; I.
RRCCPETO; ROSTER; PS01036; NEUROTR ION CHANNEL; I.
RRCCPETO; ROSTER; PS01036; NEUROTR ION CHANNEL; I.
RRCCPETO; ROSTER; RO
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                          Note=No experimental confirmation available;
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MALAV -> MGSCPL (In isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8A9EBC5D71AEC7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D -> G (IN REF. 1).

DD -> TT (IN REF. 1).

I -> S (IN REF. 1).

L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_013240.
VSLPLALSP -> ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_000073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-3 CHAIN.
                IsoId=P32297-1; Sequence=Displayed;
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BY SIMILAR
                                                                                                                                                                                                                                                                               EMBL, M86383, AAC84176.1, --
EMBL, M37981, AAA59942.1; --
EMBL, U62412, AAB40110.1; --
EMBL, Y08418, CAA69695.1, --
EMBL, AJ007784, CAA07682.1; --
EMBL, AJ007784, CAA07682.1; JOINED.
EMBL, AJ007786, CAA07682.1; JOINED.
EMBL, AJ007786, CAA07682.1; JOINED.
EMBL, BC001642, AAH01642.1; --
EMBL, BC000596, AAH0296.1; --
EMBL, BC000513, AAH00513.1; --
EMBL, AS3859, CAA37625.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VS
14 LS
100 D
100 D
235 I
430 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:1957; CHRNA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
289
326
475
495
171
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170
5
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                                                      IsoId=P32297-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A37040; A37040.
PIR; A53956; A53956.
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11
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503 AA;
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                                    Name=2
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                                                                                                         VDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAKIDLVLI
                                                                                                                                                                                             G-SSMNLKDYWESGEWAIIKAPGYKHDIKYNCCEEIYPDITYSLYIRKLPLFYTINLIIP
                                                                                                                                                                                                                                                                                SSSSESVDAVLSLSALSPEIKEAIQSVKYIAENKKAQNEAKEIQDDWKYVAMVIDRIFLW
                                                   12 APAGLILLICLIMPRGARCGYHEKRLIHHLIDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                       SPPRLLLLLLLSLLP-VARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEVSMSQLV
                                                                                              DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                       STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                          CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                                                                        AHSCFGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
                                                                                                                                                                                 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                CLLISFLTVLVFYLPSDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLLFT
                                                                                                                                                                                                                                                                     MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GSATTPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hypothalamus;
MEDLINE-97062879; PubMed-8906617;
Bliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic accetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                              30;
          503;
        Score 960; DB 1; Length 50
Pred. No. 7.9e-74;
Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 AA
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Neurosci. 7:217-228(1996)
                              90;
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Blechschmidt K., Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
       36.0%;
41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                 474 IFTLFTIIATLAVLL 488
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480 VFTLVCILGTAGLFL 494
                              Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACH2_HUMAN
Q15822; Q9HAQ3;
01-NOV-1997 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606,
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beta 4
Mol. P
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           Query Match
                    Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                                      SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE COMBINED TO BETA-4 TO GIVE.RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LCCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 YQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases-
-!--FUNCTION. AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN COMPONATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).

N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

7F512B06CCD9AAFD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
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GO:00005892; C:nicotinic acetylcholine-gated receptor-chan.

GO:0004889; F:nicotinic acetylcholine-activated cation-se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.0%; Score 960; DB 1; Length 52:38.9%; Pred. No. 8.4e-74;
Live 90; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0007165; P:signal transduction; TAS. GO:0007268; P:synaptic transmission; TAS.
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BY SIMILARITY
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CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006029; Neu_channel_membricerpro; IPR006202; Neu_channel_membricerpro; IPR006201; Neur_channel. Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1. PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U62431; AAB40109.1; -.
EMBL; Y10281; CAA76154.1; -.
EMBL; AF311103; -; NOT_ANNOTATED_CDS.
Genew; HGNC:1956; CHRNAC
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529 AA;
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199; Conserv
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265
297
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                                                                                                   MEMBRANE.
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MIM; 118502;
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us-09-303-232-4.rsp

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SIGNAL
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                                                                                                                                                                         440
::||: | | |: ::||| :: AKIDLE-QMEQTVDLKDYWESGEWAIVNATGTYNSKKYDCCAEIYPDVTYAFVIRRLPLF 267
                                                   LGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSAT
                                                                                                                                                                                                --HPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADI
                                      YFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I-FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                             TPPPARVPPPPDLELRERSSKSLLANVLD-----IDDDFR------
                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA), A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND THREE NON-ALPHA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.; "Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors."; EMBO J. 7:595-601(1988).
                                                                                                                                                                                                                                                     SRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                   528 AA
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PIR; S00377; ACCH2N.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE-88283624; PubMed=3267226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07339; CAB59645.1; -. EMBL; X07340; CAB59645.1; JOINED. EMBL; X07341; CAB59645.1; JOINED. EMBL; X07343; CAB59645.1; JOINED. EMBL; X07343; CAB59645.1; JOINED.
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07344; CAB59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBRANE.
                                                                                                                                                                                                                                                                                                                                           ACH2_CHICK
P09480;
                                                                                       304
                                                                                                                 328
                                                                                                                                             364
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                                                                                                                                                                                                                                                    457
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                                                                                                                                                                                                                                                                                                                                   ACH2_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FGVDYELSL----ILKEIRVITDQMRKDDEDADISRDWKFA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 GKASGGPAPQVPLKGEEVGSDQGLTLSPSILRALEGVQYIADHLRAEDADFSVKEDWKYV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 GFAEDRLFKHLFTGYNRWSRPVPNTSDVVIVKFGLSIAQLIDVDEKNOMMTTNVWLKQEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 EKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-----PPPDLELRERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 SRCWLET - - DVDDKWEEEEEEEEEEEEEERAYPSRVPSGGSO - - - GTQCHYSCERQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 NAIGRYNSKKYDCCTEIYPDITFYFVIRRLPLFYTINLIIPCLLISCLTVLVFYLPSDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKSLLANVLDIDDDFRHPQAQQPQ------CCRYYRGGEENGAGLAAH-SC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                      NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Gaps
                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                             (BI SIMILARIII).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E76C6360AF876364 CRC64;
            Pfam: PF02931; Neur_chan_LBD; 1.
Pfam: PF02932; Neur_chan_LBD; 1.
Pfam: PF02932; Neur_chan_memb; 1.
TIGRPAMS; TIGROOGO, LIC; 1.
PROSTIE; PS00236; NEUROTR, ION_CHANNEL, 1.
PROSTIE; PS00236; NEUROTR, ION_CHANNEL, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%; Score 959; DB 1; Length 52: 39.2%; Pred. No. 1e-73; Live 84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACH1_DROME STANDARD; PRT; 567 AA. P09478, 99074; 01-MAR-1989 (Rel. 10, Created) 15-SEP-2003 (Rel. 42, Last sequence update)
                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                        ALPHA-2 CHAIN
EXTRACELLULAR
                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AMVVDRLCLIIFTLFTIIATLAVLL 488
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                                                                                                                                  Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                             60675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.0°
Best Local Similarity 39.2
Matches 198; Conservative
                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                                         528 AA;
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158
222
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DISULFID
DISULFID
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SEQUENCE
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TRANSMEM
TRANSMEM
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TRANSMEM
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RAY AGAINS M.D. Celluker S.E. I. P.W. Broakins R.A., Galle R.F.,

Adams M.D., Celluker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams W.D., Celluker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Broakins R.A., Galle R.F.,

Ray Corress R.A., Lewis S.E., Holt R.A., Evans G., Chan L.X.,

Button G.G., Worthan J.R., Yandell M.D., Zhang G., Chan L.X.,

RA Bardon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Peleifers B.D.,

RA Man K.H., Doyle C., Baxer B.G., Helt G., Champe M., Peleifers B.D.,

RA Bardon R.C., Rogers Y.H.C., Helt G., Champe M., Peleifers B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Gaver B.C., Butter R., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A.,

Buttis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Buttis K.J., Evangelista C.C., Ferrac C., Ferrac S., Pleischmann W.,

RA Podson K., Doup L.E., Downes M., Dugan-Rochs S., Dunky B.C., Dunn P.,

Buttin K.J., Evangelista C.C., Ferrac C., Ferrac S., Reniss M.,

Ray Dodson K., Doup L.E., Gorrell J.H., Gu Z., Gan P., Harris M.,

Ray Liu X., Martel B.E., Gorrell J.H., Gu Z., Gan P., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

Alalali M., Kalush F., Karpen G.H., Ke Z., Gan M.P., Merperson D.,

RA Harris N. Mattel B. McIncosh T.C., Moriecu M.P., Merperson D.,

RA Mexidnow G., Milalaina N.V., Mobarry C., Moriso, W. N., Nelson D.L.,

RA Blazzolo M., Pittman G.S., Pan S., Pollard J., Pull, Y., Reses M.

Reinert K., Reiniqton K.A., Nixon K., Nixon K., Wary D.M., Nelson D.L.,

Ray Blazzolo M., Pittman G.S., Pan S., Pollard J., Wang S., Yao Q.A.,

RA Mang Z.-Y., Massarman D.A., Weinstock G.M., Weisenbach J.,

Ray Reinert K., Spradling A.C., Stapleton M., Stupsk W. Smith T.,

Spier E., Spradling A.C., Stapleton M., Shong W., Smith H.O.,

Ray Reinert K., Reinert E., Stan M., Shong W., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systematic review ":
enome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
                                                                                                                                                                                        MEDLINE-88283626; PubMed-2840281;
Bossy B., Ballivet M., Spierer P.;
"Conservation of neural nicotinic acetylcholine receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome:
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
MAGR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopteraygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                              Drosophila to vertebrate central nervous systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                EMBO J. 7:611-618(1988).
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                       Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis S.
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                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 QLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: CNS IN EMBRYOS. DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 VVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL---QLQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 ---EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PROQUSS6; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family; Polymorphism.
SIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLCHOLINE RECEPTOR PROTEIN, ALPHALIKE CHAIN 1. EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

Y -> H (IN REF. 1).
                                                                                                                                                          SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> H.
-> H (IN REF. 1).
08E1F721FB2A92AC CRC64;
                                                                   membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.9%; Score 956.5; DB 1
38.2%; Pred. No. 1.8e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC.
                                                                 Integral memb
S IN EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003747; AAF56301.2; -. PIR; S00381; ACFFA1.
FlyBase; FB900000036; nAcR-alpha-96Aa.
InterPro; IPR006202; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF02931; Neur_chan_LBD; 1.
Pfam: PF02932; Neur_chan_memb; 1.
PRINTS: PR00252; NRIONHANNEL.
TIGRPAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64019 MW;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07194; CAA30172.1; -.
                                                                   SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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538
108
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                                                                                                                                       LARVAE STAGES
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                                            MEMBRANE
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DISULFID
DISULFID
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CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                                                                                    426
CIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPAR 369
                                                                                                               ANVLDI --- DDDFRHPQAQ ---- QPQCCRYYRGGEENGAGLAAHS ---- CFGVDY -- ELS 434
                                                                                                                                          427 PSSLPLPGADDDLFSPSGLNGDISPGCC-----PAAAAAAADLSPTFEXPYAREME 478
                                                                                                                                                                      LILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHI 493
                                                                                                                                                                                     SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA (BETA), ALPHA-2 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LCCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                | :| ||| || :|| :| :| || || :| || FTWMLVTLSVVVTIAVLNVFRSPVTHRMAPWVQRLFIQILPKLLCIERP--KKEEPEED
                                                                                  367 OPPEVLTDVYHLPPDVDKFVNYDSKRFSGDYGIPALPASHRFDLAAAGGISAHCFAEPPL
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boulter J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Brain; MabLine-Ballalis; PubMed-2813952; MabLine-Ballalis; PubMed-2813952; Mada K., Ballivet M., Boulter J., Connolly J.G., Wada E., Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.; Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor."; Science 240:330-334(1988).
                                                                                                                                                                                                                                                                                  p12389; 008952;
01-027-1989 (Rel. 12, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                        511 AA
                                                       VPP-----PPDLE-LRERSSKSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006029; Neu_channel_memb
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 KNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 KNOMMTINVWIKQEWNDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGEFAVTHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TKAHLFFTGTVHWVPPAIYKSSCSIDVTFFPFDQQNCKMKFGSWTYDKAKIDLE-QMERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 SCLTVLVFYLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 ·TLSIVITVFVLNVHHRSPSTHNMPNWVRVALLGRVPRWLMMNRP-----LPPMELHGSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 LKL--SPSYHWLETNMDAGEREETEEEEEE-----DENICVCAGL-PDSSMGVLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ELSLILKEIRVITDQMRKDDEDADISRDWKFAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 ASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARVPPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEEN---GAGLAAHSCFGVDY-
                                                                                                                                NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN. EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Gaps
                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
C -> S (IN REF. 1; AAA40664).
3824E83BB01D613B CRC64;
              Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITSpraptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 951; DB 1; 39.4%; Pred. No. 4.7e-73;
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(Rel. 30, Last sequence update)
                                                                                                                                                                                                                                                                                        SIMILARITY
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POTENTIAL.
POLY-GLU.
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VVDRIFLWLFIIVCFLGTIGLFL
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Pfam; PF02931; Neur_chan_LBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              58611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 39.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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329
484
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242
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01-OCT-1994
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Q07263;
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DOMAIN
DISULFID
DISULFID
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417

294

467

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245 FFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL 304
                                                                                                                                                                     SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE
                                                                                                               185 QLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYY
                                                         GTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----G
                                                                                                                                                                                                               SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN-
                                                                                                                                                                                                                                         355 NTQRPRPFYSAELSNLNCFSRIESKVCKEGYPCQDGL------CGYCHHRRAKISNF
                                                                                                                                                                                                                                                                      GAGLA-AHSCFGVDYELSL------ILKEIRVITDQMRKDDEDADISRDWKFAAMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86118671; PubMed=3753746;
Boulter J., Evans K., Goldman D.J., Martin G., Treco
Heinemann S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                            499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                             DRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=88041184; PubMed=2444984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94193711; PubMed=8144606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                        305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDORCEMKFGSWTYDGY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                          FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                 Sequence FROM N.A.

MEDLINE-92319195; PubMed=1620271;

Criado M., Alamo L., Navarro A.;

Criado M., Alamo L., Navarro A.;

"Primary structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";

acetylcholine receptor from bovine adrenal chromaffin cells.";

acetylcholine Res. 17:281-287(1992).
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

(BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
 28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor
                                                                                                                                                                                                                                                                     SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 936.5; DB 1;
Pred. No. 7.7e-72;
9; Mismatches 181;
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; Neur_chan_memb; 1.
IGRPAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
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39.5%;
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Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
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163
214
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                                                                                   Bovinae; Bos
                                       taurus (Bovine).
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162
195 AA;
                                                                                                NCBI_TaxID=9913;
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263
296
319
468
149
213
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28-FEB-2003
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CARBOHYD
SEQUENCE
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                                                                                   Bovidae;
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S.F., Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus. "Characterization of an acetylcholine receptor alpha 3 gene promoter and its activation by the POU domain factor SCIP/Tst-1.";
J. Blol. Chem. 269:10252-10264(1994).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA Patrick J.; Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor alpha-subunit."; Nature 319:368-374(1986). Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor "Functional expression of two neuronal nicotinic acetylcholine receptors from cDNA clones identifies a gene family."; Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987). Yang X., McDonough J., Fyodorov D., Morris M., Wang F., Deneris E.S.; ä

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 FDSTYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIMFMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSAT-TPPPA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 FIMIFVILSIVITVFVLNVHYRTPTTHTMPTWVKAVFLNLLPRVMFMTRPTSGEGDTPKT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVPPPPDLE----LRERSSKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN-GAGL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQ
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
               LOCATION: Integral membrane protein.
BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
D66C491E832B9C34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
                                                                                                                                                                                                                  InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006209; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; Neur_chan_memb; 1.
IIGRNAS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Multigene family SIGNAL 1 25 POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 N
56997 MW;
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322
471
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166
499 AA;
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                            SIMILARITY:
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414 TRSSSSESVNAVLSLSALSPEIKEAIQSVKYIAENMKAQNVAKEIQDDWKYVAMVIDRIF 473
------AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLC 471
                                                                                           472 LIIFTLFTIIATLAVUL 488
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474 LWVFILVCILGTAGLFL 490
422
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Search completed: August 13, 2003, 15:26:11 Job time : 11.386 secs

pp

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:21:45; Search time 18.5263 Seconds (without alignments) 2574.698 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-4 2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHINVS 496

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nicotinic acetylch	alpha 7 neuronal n	nicotinic acetylch	nicotinic acetylch	nicotinic receptor	alpha-bungarotoxin	nicotinic acetylch				ace	nicotinic acetylch		nicotinic acetylch				nicotinic acetylch		nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch				
SUMMARIES	ΩI	JN0113	G02259	ACHUA7	A57175	T01378	JH0173	86888	T25671	T19622	T19862	S12359	A53956	ACCH2N	ACFFA1	A37040	A40110	860589	A24572	ACFFA2	ACCHAN	ACCHNN	ACCH4N	G02421	S10505	I50548	JH0174	T09289	ACRYA1	B37014
	DB	7	7	Н	7	7	7	7	7	~	7	7	7	Н	-	7	~	7	~	Н	-	-	П	~	~	7	7	7	7	7
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æ	Query	47.5	46.6	46.6	46.6	46.2	45.8	45.1	42.8	39.8	39.6	36.7	36.1	36.0	35.9	35.8	35.8	35.1	35.0	34.7	34.5	34.1	33.9	33.9	33.9	33.8	33.8	33.8	33.7	33.7
	Score	1267	1242	1241	1241	1232.5	1219.5	1201	1141	1060	1055.5	979	962	959	957.5	954	953	936.5	932	926	918.5	908.5	904	903.5	902.5	902	901	900.5	æ	898.5
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nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	probable nicotinic	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	hypothetical prote	nicotinic acetylch	nicotinic acetylch	hypothetical prote	
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495	457	200	457	457	470	445	457	517	459	627	457	468	521	625	265	
33.7	33.6	33.5	33.4	33.4	33.3	33.3	33.2	33.2	33.2	33.0	32.9	32.9	32.8	32.8	32.6	
868	896.5	892.5	890	688	888	887	886	988	885.5	879.5	876.5	875.5	875	874	869	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

	RESULT 1. JN0113 niootinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
	N'ALCELINGE HOMBES: alpha Punigationali binding process aspina chain C.Species: Gallus gallus (chicken) C.Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
	C;Accession: JN0113; JH0172; S28018; B25738; S26566 R;Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N
	Neuron 5, 847-856, 1990 A,Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
	A;Reference number: JN0113; MUID:91097796; PMID:1702646 A;Accession: JN0113
	A;Cross-references: GB:X68586; NID:9287756; PIDN:CAA48576.1; PID:9287757 A:Experimental source: white leghorn: brain
	R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990
	A; Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of the Reference number: IHO170: MITD: 40115158. DMID: 2369519
	A; Accession: JH0172
	A;Molecule type: mRNA A;Residues: 1-502 <sch></sch>
	A;Cross-references: EMBL:X52295; NID:963077; PIDN:CAA36543.1; PID:963078
	A; Experimental source: Drain R; Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.
	EMBO J. 11, 4529-4538, 1992
	A;Title: Neuronal specificity of the alpha/ nicotinic acetylcholine receptor promoter A:Reference number: S28018; MUID:93049204; PMID:1425587
	A; Accession: S28018
	A; Molecule type: DNA A; Residues: 1-18 <mas></mas>
	A,Cross_references: EMBL;X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
	A; Experimental source: white leghorn; erythrocyte R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
	Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
	Ajricie: Brain and muscie nicocinic acetylcholine recepcors are different but nomolog A;Reference number: A94055; MUID:85270494; PMID:3860855
	A, Accession: B25738
	A. MOLECULE (1795 - DIOLEII) A. Residines: 24-25, Fgr. 28-41, X', 43-45, X', 47 <con></con>
	C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
	C;Genetics: A;Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
	C; Superfamily: acetylcholine receptor
	C; Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote F:1-23/Domain: signal sequence #status predicted <sig></sig>
	24-502/Product:
	F:261-280/Domain: transmembrane #status predicted <fr. F:262-280/Domain: transmembrane #status predicted <fr2></fr2></fr. 
	296-317/Domain: transmembrane 470-488/Domain: transmembrane
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us-09-303-232-4.rpr

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carbohydrate (Asn) (covalent) #status predicted
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C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C; Accession: G02259
R; Leonard, S.
submitted to the EMBL Data Library, November 1995
A; Reference number: H00936
A; Accession: G02259
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
                                                                                                                                                                                                                                                                                                                                                                                    YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                             GVICGRATCSPTEEENLLHSGHPSEG-DPDLAKILEEVRYIANRFRDQDEEEAICNEWKF
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                                                                                                                                                               LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV
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                                                                                                                 Gaps
                                                                                                                 36;
    F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status p
F;365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #s
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.6%; Score 1242; DB 2; 46.0%; Pred. No. 2.8e-100;
                                                                                                                 Mismatches 144;
                                                                                Score 1267; DB 2;
Pred. No. 1.9e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-502 <LED>
A;Cross-references: EMBL:U40583; NID:91125076; PIDN:
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                              83;
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                                                                                47.5%;
                                                                                                Best Local Similarity 48.69
Matches 249; Conservative
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Amap position: 15q14-15q14

A;Note: defects in this gene have been associated with mental retardation and schizop c;Complex: the functional receptor molecule is a heteropentamer with two alpha chains c;Complex: the functional receptor

C;Complex: the functional receptor

C;Complex: the functional receptor

C;Reywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor

F;1-23/Domain; signal sequence #status predicted <IRI>
F;24-50/Domain: transmembrane #status predicted <IRI>
F;26-28/Domain: transmembrane #status predicted <IRI>
F;26-31/Domain: transmembrane #status predicted <IRI>
F;40-488/Domain: transmembrane #status predicted <IRI>
F;40-488/Domain: transmembrane #status predicted <IRI>
F;40-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Reference number: A54194; MUID:94245214; PMID:8188270
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A;Molecule type: mRNA
A;Residues: 1-502 <PEN>
A;Residues: 1-502 <PEN>
A;Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607
A;Experimental source: brain neuroblastoma cell line SHSY-5Y
B;Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, Genomics 19, 379-381, 1994
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C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Micotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human Nicotinic acetylcholine receptor alpha-7 chain Cispecies: Homo sapiens (man) Cispecies: Natz Man, Micotinic Evolution (man) Cispecies: Natz Man, Gerzanich, V.; Anand, R.; Lindstrom, J. Ripermacol. 45, 546-554, 1994 Mol. Pharmacol. 45, 546-554, 1994 A; Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subuniomers expressed in Xenopus oocytes.

A; Reference number: 137185
                                                                                                                                                                                                                                                              361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                      CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DEHLLH-----GGQPPEG------DPDLAKILEEVRYIANRFRCQDE
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Modecule type: mRNA
A; Residues: 24 363, 'S', 365-374,'A', 376-408,'AWPAP', 414-502 <CHI>
A; Cross-references: GB: 223141; NID: 9457736; PIDN: CAA80672.1; PID: 9457737
                                                                                                                                                                                                                                                                                                                                                      312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
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nicotinic receptor alpha 7 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 12-Peb-1999 #sequence\_revision 12-Peb-1999 #text\_change 21-Jul-2000
C;Accession: T01378
R;Sequela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A;Title: Molecular cloning, functional properties, and distribution of rat brain alph A;Reference number: 214310; MUID:93147931; PMID:7678857
A;Accession: T01378
A;Status: preliminary; translated from GB/EMBL/DDBJ ë 112 180 172 240 229 300 289 360 349 415 æ 120 398 ---ENGAGLAAHSCFGV-----DYELSLILKEIRVITDQMRKDDEDADISR 458 PIPDSGVVCGRLACSPTHDEHLMHGTHPSDGDPDLAKILEEVRYIANRFRCQDESEVICS 458 113 181 9 SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL 121 52 53 61 A;Cross-references: EMBL:553987; NID:9264770; PIDN:AAB25224.2; PID:95705903 A;Experimental source: brain C;Superfamily: acetylcholine receptor LSFGLTLMQIIDVDEKNQLLTTNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 241 TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 301 VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG 1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE-----EDKVRPACQHKP------RRCSLASV-ELSAGAGPPTSNGNLLYIGFRGLEGMHCA 2 GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL 122 MYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTY 49; Length 502, Length 502; Indels DB 2; DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494 :||||| |||||||| : |:|||| |: ||||| : EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 141; Mismatches 139; Pred. No. 3.4e-100; Query Match 46.2%; Score 1232.5; DB Best Local Similarity 47.2%; Pred. No. 1.9e-99; Matches 244; Conservative 83; Mismatches 141 46.6%; Score 1241; 47.1%; Pred. No. 3. :06 Conservative Best Local Similarity Matches 243; Conserv A; Molecule type: mRNA A; Residues: 1-502 <SEG> 61 113 121 181 361 459 459 62 Query Match RESULT 5 δ Op à ρp δ g ò g δ g δ qq QY g ò qq δ . B δλ g ŏ a ò Genomics 26, 399-402, 1995

A;Title: Cloning and mapping of the mouse alpha?-neuronal nicotinic acetylcholine recept
A;Reference number: A57175; MUID:95324936; PMID:7601470
A;Accession: A57175 9 452 191 12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71 :| |: | | : | : | ::| |::|| SPGGVWLGLAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 20-Aug-1999 DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI -----SATTPPPAR-------VPPPPDLELRERSSKSLLANVLD QRRCSLASVEMSAVGPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE Gaps A;Cross-references: GB:L37663; NID:9790853; PIDN:AAC42053.1; PID:9790854 C;Superfamily: acetylcholine receptor F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted F:415/Binding site: phosphate (Thr) (covalent) #status predicted F:442/Binding site: phosphate (Tyr) (covalent) #status predicted 70; Length 502; MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG Indels DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494 SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 R;Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L. 126; 46.6%; Score 1241; DB 1; 46.0%; Pred. No. 3.4e-100; tive 86; Mismatches 126; F;150-164/Disulfide bonds: #status predicted Best Local Similarity \*0.00 Matches 240; Conservative A; Molecule type: mRNA A; Residues: 1-502 <ORR> -DEHLLH-A;Status: preliminary C; Accession: A57175 Query Match 72 132 124 192 184 252 241 312 301 361 361 393 453 RESULT 쉽 рp q g g õ ò ò q ç ò ò g ò ð g ò a

Db 193ADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC 249  253 VLIASMALLGETLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312	RESULT 7 8ESULT 7 8ESULT 7 868508 nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) . Caenorhabditi C:Species: Caenorhabditis elegans activated by the company of the	137   NVVVRNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG   196   1:1
114	Oy 458 RWWFRANUVDRECLIFFIFTIRATLAVLLSAPHIM 494  bb 458 SEWRFAACVVDPLCIMAFSVFTITCTIGILMSAPNEV 494  RESULT 6  JH0171  SERVIT CATGLIMSAPNEV 494  RESULT 6  JH0171  JH0171  JH0171  RESULT 6  JH0171  JH0171  JH0171  RESULT 6  JH0171  JH0171  JH0172  JH0173  JH	Query Match         45.8%; Score 1219.5; DB 2; Length 511;           Best Local Similarity         46.3%; Pred. No. 2.7e-98;           Matches 236; Conservative 88; Mismatches 131; Indels 55; Gaps 9;           Qy         20 LCLLWPRGARGGYHEKRLLHHLDHYNVLERPVNNESDPLOLSFGLTLMQIID 72           11 LC-LMASLFLSFFWXSQGESGRRLYRDLRNYNRLERPVNNDSQPLVVELQLSLLQIID 72           Db         14 LC-LMASLFLSFFWXSQGESGRRLYRDLRNYNRLERPVNNDSQPLVVELQLSLLQIID 72           Qy         73 VDEKNQLLITNIMLKLEWNDMNLRNMTSDFGGVNDLRVPPHRLMKPDVLMYNSADEGRDS 132           PDb         73 VDEKNQLLITNAMLQMYWDIYLSWDQYEYPGVQNLRFPSDQINVPDILLYNSADERFDA 132           Qy         133 TYPTNVVNRNGSCLYVPPGIFKSTCXIDTWFPFDDQRCEMKFGSWTYDGYQLDLQLQD 192           PD         133 TYPTNVVNNYSGSCQYIPPGILKSTCYIDVRWFPFDVQKCLKFGSWTHSGWLIDLQMLE 192           Qy         193 EGGGDISSFVTNGSWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRYLYYFFNLIVPC 252           Qy         193 EGGGDISSFVTNGSWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRYLLYYFFNLIVPC 252

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RESULT 10
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C;Species: Caenorhabditis elegans
C;Accession: T25671
R;Gattung, S.; Maggi, L.
Submitted to the EMBL Data Library, February 1997
A;Reference number: Z20067
A;Reference number: Z20067
A;Reference number: Z20067
A;Accession: T25671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-461 <GAT>
A;Coss-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A;Experimental source: strain Bristol N2; clone D2092
                         94 NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILN 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 YHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPDLELRERSSKSLL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLIL-----KEIRV 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 ETKLFTDLLKGYNPLERPVQNSSQPLEVKIKLFLQQILDVDEKNQIVSVNAMLSYTWFDH 85
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A;Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1141; DB 2; Length 46; Pred. No. 1.6e-91; 85; Mismatches 121; Indels
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FTIFIIVSTIGIFWSAPYLV 497
                                                                                         FTLFTIIATLAVLLSAPHIM 494
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Best Local Similarity 46.2%;
Matches 218; Conservative 8
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hypothetical protein C31H5.3 - Caenorhabditis elegans

RESULT 9 T19622

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kershaw, J.
submitted to the EMBL Data Library, April 1997
A; Reference number: 219153
A; Accession: T19622
A; Accession: T19622
A; Accession: T1962
A; Accession: T1962
A; Status: prealiminary; translated from GB/EMBL/DDBJ
A; Residues: 1-560 <WIL>
A; Residues: 1-560 <WIL>
A; Residues: BmBL:293778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3
A; Experimental source: clone C31H5
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: : ! !
. : : SUBARASDNKKKQRQYLIEVERHILTRPNGNGHSAVDKAVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LLLLLCLLWPRGARC-----GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIDVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTPPPARVPPPDLEL-----RERSSKSLLANV-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 DLSTGNPHSDAKKSSPSPKRTSASIMGMTGLPTTQMNGALDSSINKYTCTKVTRPLENGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQDEGGGDISSFVT-----NGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                         Length 560;
                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || || || : || || : | : | : | : | || DWMFASRVVDRVCFLAFSAFLFMCTAIISYNAPHLFV 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMV 495
                                                                                                                                                                                                                                                                                                                                                                                     39.8%; Score 1060; DB 2; 37.6%; Pred. No. 2.5e-84; Live 96; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Accession: T19862
R; Hembry, C.
submitted to the EMBL Data Library, March 1996
A; Reference number: Z19188
A; Accession: T19862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIDDDFRHPQAQQPQ---
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.6%
Matches 217; Conservative
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                                                                                                                                                                                                                                                                             A; Gene: CESP:C31H5.3
                                        C; Accession: T19622
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predicted

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F:47,235/Binding site: carbohydrate (Asn) (covalent) #status
         F;501-523/Domain: transmembrane #status predicted <TM4>
                                                                 36.7%;
                                                                                   Best_Local Similarity 40.0
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Schistocerca gregaria (desert locust)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C; Accession: 512359
R; Marshall, J; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
A; Titles: Sequence and functional expression of a single alpha subunit of an insect nicot A; Reference number: 512359; MUID:91092263; PMID:1702381
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rosldues: 1-542 <WIL>
A;Cross-references: EMBL:270266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.2
A;Map position: X
A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-----SATTPPPA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 PRVTYSKVMAESYVEDVVMTELNKYMQ------KACL----ELKNISSQTRAMRK 492
                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GEWNLLAVPARHETNIFD--EQPYPSLFFYLLIQRRTLYYGLNLIIPSFLISLMTVLGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 KQGSIKNGVGPGKPTDSVHPSEGLSLMKNIKLGRQQTIDFEYEFHVQHNHLMPVAPSEMT
                                                                                                                                                                                                                                                                                                                                                                    94 NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ-----DEGGGDISSFVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL-----GTYFNCIMFMVASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RV-----PPPPDLELRERSSKSLLANV-----LDIDDDF--RH-----PQAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITD
                                                                                                                                                                                                                                                                                               34 EKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFT
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         icotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134 C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                    Length 542;
                                                                                                                                                                                                                                             -84;
136; Indels
                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                    Score 1055.5; DE
Pred. No. 5.9e-84
                                                                                                                                                                                                                  Query Match 39.6%; Score 1055.5; Best Local Similarity 40.5%; Pred. No. 5.9e-Matches 214; Conservative 94; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-557 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
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nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 20-Aug-1999
C; Accession: A53956; S21338
R; Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A; Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuro A; Reference number: A53956; MUD:9114756; PMID:1989896
A; Reference number: A53956; MUD:9114756; PMID:1989896
A; Residues: 1-503 < MIH>
A; Residues: 1-503 < MIH>
A; Residues: 1-503 < MIH>
A; Residues: Lindstrom, J Library, June 1990
A; Cross-references: GB:M37981; NID:9189252; PIDN:AAA59942.1; PID:9189253
R; Anand, R; Lindstrom, J Library, June 1990
A; Description: Nucleotide sequence of the mature human nicotinic acetylcholine recept A; Reference number: S21338
A; Accession: S21338
A; Residues: 30-503 < ANA>
A; Cross-references: EMBL:X53559; NID:934986; PIDN:CAA37625.1; PID:934986
C; Genetics:
                                                                10;
                                                                                                                                                                                                                                                          IDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||||||||| |: :::| | || |||||||:||| |:||| |:| :::| :|||| |:|
FYTVNLIVPCYGISYLSVLVFYLPADSGEKIALCISILLSQTWFFLLISBIIPSTSLALP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
                                                                                                                                                                                                                                                                                                                                                                                                                            LLGTYFNCIMFWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YELSLILKEIRVITDQMRKDDE-DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AAPAGLILLICTIUWPRGARCGYHEKRLIHHLLDHYNVLERPVVNESDPLQLSFGLTLMQI 70
                                                                                                                                                                                         63
                                                                                                                                                                     ALPPMLILLLLLLLLHHPAAANPDAKRLYDDLLSNYNRLIRPVSNNTDTVLVKLGLRLSQL
                                                                                                                                                                                                                                                                                                     DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPPPARVPPPDLELRERSSKSLL--------ANVLDIDDDFRHPQ
                                                                   Gaps
                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SCFGVD--
                                                                Indels
                                                                88; Mismatches 160;
Score 979; DB 2;
Pred. No. 2.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 AQQPQCCRY----YRGGEENGAGLAAH-----
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10;

90 90 269

329

380 426 435 463

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nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila mela C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002 C; Accession: S00381; A38801 R; Bossy, B.; Ballivet, M.; Spierer, P. EMBO J. 7, 611-618, 1988 A; Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to A; Reference number: S00381; MUID:88283626; PMID:2840281 A; Accession: S00381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:nAcR-alpha-96Aa
A;Cross-references: FlyBase:FBgn000036
A;Cross-references: FlyBase:FBgn000036
A;Map position: 3R 96A
A;Map position: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted
F;240-264/Domain: transmembrane #status predicted <TMT>
F;240-264/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                           NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP 150
                                                                                                                                                                                                                                                                                                                                                      EKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-----PPPDLELRERS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1 | 1 | 1 | 1 | 1 | 1 | 436 GKASGGPAPQVPLKGEEVGSDQGLTLSPSILRALEGVQYIADHLRAEDADFSVKEDWKYV 495
                                                                                                                                                                                                                                                                          91 SDYKLRWNPEDFDNVTSIRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSNGKVKWVP 150
                                                                                                                          31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                    GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 NAIGRYNSKKYDCCTEIYPDITFYFVIRRLPLFYTINLIIPCLLISCLTVLVFYLPSDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------FGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFA
                                                                                                                                                                                                                                                                                                                              PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CCRYYRGGEENGAGLAAH-SC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residudes: 1-567 -802.
A; Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A; Note: 538-Tyr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:X07194; NID:q7575; PIDN:CAA30172.1; PID:g7576
                                                                           62;
                            Length 528
                          ; DB 1;
1.5e-75;
                                                    Pred. No. 1.5e
84; Mismatches
                          36.0%; Score 959; 39.2%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AMVVDRLCLIIFTLFTIIATLAVLL 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.09
Best Local Similarity 39.29
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-567 <BOS>
A; Cross-references: GB:3
A; Accession: A38801
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C. Superfamily: acetylcholine receptor
C. Keywords: glycoprotein; lon channel; neurotransmitter receptor; postsynaptic membrane;
C. F.1-23/Domain: signal sequence #status predicted <SIG>
C. 24-528/Product: nicotinic acetylcholine receptor Tabha-2 chain #status predicted <MAT>
C. 24-528/Promain: transmembrane #status predicted <TML>
C. 272-290/Domain: transmembrane #status predicted <TML>
C. 272-290/Domain: transmembrane #status predicted <TML>
C. 506-520/Domain: transmembrane #status predicted <TML>
C. 507-520/Domain: transmembrane #status predicted <TML>
C. 508-520/Domain: transmembrane #status predicted <TML>
C. 522-223/Dissulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nicotinic acetylcho
                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                   66 TLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNLIVPCVLIASMALLGFTLPPDSGEKĻSLGVTILLSLTVFLNMVAETMPATSDAVPLLG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 EYLLFTMIEVTLSIVITVFVLNVHYRTPTTHTMPSWVKTVFLNLLPRVMFMTRPTSNEGN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 AQKPRPLYGAELSNLNCFSRAESKGCKEG------YP-CQDGMCGYCHHRRIKISNF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 SANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVI 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTPPPARVPPPDLELRERS-SKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN- 417
                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S00377
                                                                                                                                                                                                                                                                                                                                                                                  :: |:: ||| ||:: ||:|| ||: ||:|| || ||:|| ||:|| ||:||| ||:||| ||:||| ||:||| ||:||| ||:||| ||:||| ||:||| ||:||| ||:|||| ||:||||| SMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWNPSDYGGAEFMRVPAQKIWKPDIVLYNN
                                                                                                                                                                                                                                                                               TYFNCIMEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFAAMVV
                                                                                                                                                                                                                                                  10 LAAPAG----LLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGL
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A;Residues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
                                                                                                                                                                                                   Gaps
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A;Title: Genes expressed in the brain define three distinct neuronal A;Reference number: S00376; MUID:88283624; PMID:3267226
A;Reference number: S00377
                                                                                                                                                                                                   34;
                                                                                                                                               Length 503;
                                                                                                                                                                                                 89; Mismatches 172; Indels
                                                                                                                                                    ; DB 2;
7.7e-76;
                                                                                                                                               Score 962;
Pred. No. 7
                          GDB:125219; OMIM:118503
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DRIFLWVFTLVCILGTAGLFL 494
                                            A; Map position: 15q24-15q24
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
                                                                                                                                                    36.1%;
                                                                                                                                                                    41.18;
                                                                                                                                                                         Best Local Similarity 41.1
Matches 206; Conservative
GDB: CHRNA3
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                                                                                                                                                                                                                                                                                                                                                                                        192
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                                                                                                                                                                                                                                                                                                  78 OLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 ANVLDI---DDDFRHPQAQ----QPQCCRYYRGGEENGAGLAAHS----CFGVDY--ELS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSSLPLPGADDDLFSPSGLNGDISPGCC-----PAAAAAAADLSPTFEKPYAREME 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537
                                                                                                                                                                                                              18 LLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN
                                                                                                                                                                                                                                         VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN
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                                                                                                                                                                                                                                                                                                                                                                                      VVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL----QLQD-
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                      F;326-513/Domain: intracellular #status predicted <INT>
F;514-532/Domain: transmembrane #status predicted <TM4>
F;45,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;149-163;222-223/Disulfide bonds: #status predicted
                                                                                                                                                                         73;
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                                                                                                                                                                         Indels
F;306-325/Domain: transmembrane #status predicted <TM3>F;326-513/Domain: intracellular #status predicted <INT>
                                                                                                                               DB 1;
                                                                                                                                                                       86; Mismatches 174;
                                                                                                                             35.9%; Score 957.5; DB 1
38.2%; Pred. No. 2.2e-75;
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Best Local Similarity 40.81
Matches 203; Conservative
                                                                                                                             Query Match 35.9
Best Local Similarity 38.2
Matches 206; Conservative
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A; Residues: 1-502 <FOR>
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FDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ 189
                                                                           306
                                                                                                                                                                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                                                                                                                               : | || :|| :|| :|| 417 TRSSSESVDAVVSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVIDRIF 476
                                                                                                                                                                               VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
                                                                                                                                                                                                                                           310 CIMEMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GSATTP 365
                                                                                                                                                                                                                                                                                                     366 PPARVPPPDLELRERS-SKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN-GAGL 421
                                                                                                                                                                                                 IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG
                                                                                                                                     A-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLC
                                                                                                                     LODEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI
                                                                                                                                                                                                                                                                                                                                   RPLYGAELSNLNCFSRAESKGCKEG -----YP-CODGMCGYCHHRRIKISNFSANL
                                                                                                                                                                                                                                                                                                                                                                                                                         472 LIIFTLFTIIATLAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 LWVFTLVCILGTAGLFL
20
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Search completed: August 13, 2003, 15:30:21 Job time : 20.5263 secs. Mature cell surfac Drosophila melanog Modified acetylcho Neuronal nicotinic

Human neuronal nic Alpha 2 subunit of Neuronal nicotinic Human neuronal NAC Human neuronal nic Modified acetylcho Modified hen ACR s Drosophila melanog

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Human neuronal NAC

Wild-type human

Nicotinic acetylch

protein

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Run on:

Sequence:

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
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AAB50016
AAB50017
AAW12369
AAE12824
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                                                                                              WPI; 2000-014207/02.
N-PSDB; AAZ24476.
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(FARB ) BAYER AG.
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Human neuronal nic
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H. virescens acety
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1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Human mutant neuro Modified acetylcho Modified hen ACR s Neuronal nicotinic

Schulte T;

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Adamczewski M, Oellers N,
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                                     acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved information of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
                              encoding a nicotinic
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                                                                                                                                                                     / Match 100.0%; Score 2665; DB 21; Length 496; Local Similarity 100.0%; Pred. No. 2.9e-258; les 496; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. melanogaster acetyl-choline receptor protein from clone Da7
                            This invention describes a novel nucleic acid (NA)
         26pp; German.
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insectlicide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
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New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
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70.0%; Pred. No. 3.3e-176;
ive 30; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS
                                                                              Example 1a; Page 12-14; 26pp; German
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414

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241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), and the encoded proteins
                                                       312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARV-
                                                                                                                                                                                      ----EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRL
                                                                                                               371 PPPPDLELRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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2000US-0614150.
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N-PSDB; ABL07786.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                        Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
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                                                                                                                                                                                    acetyl-choline receptor protein from clone Hva7-2.
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Pred. No. 8.2e-172;
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                                                                     AAY50816 standard; Protein; 501 AA.
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N-PSDB; AAZ24477.
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                                                                                                                                                                                    H. virescens
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ABB60432 standard; Protein; 498
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                                                                                     al Similarity 48.6
249; Conservative
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                                                            502 AA;
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11-JUL-2000;
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                                                    SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL
                                                                            MYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTY
                                                                                      LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
        GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL
                                                                                                               DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                            al alpha-bungarotoxin binding protein alpha 1; cholinergic; binding; ion channel.
                                                                                                                                                                                                                                                                                                Neuronal alpha-bungarotoxin binding protein alphal subunit.
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/label= Mat_protein
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N-PSDB; AAT59196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMYNSADEGFDSTYPTNVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 PQCCRYYRGG--EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intac ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 8088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%; Score 1267; DB 18;
48.6%; Pred. No. 5.6e:118;
iive 83; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 SATTPPPARVPPPDLELRERSSKSLLANVLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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187 DLQLQDEGGGDISSFVTNGEWELIGV-PGK-------RNEIYYNCCPEPYIDI 231
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                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWVASSVVST1L1LNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGFDSTYPTNVVVRNNGSCLYVPPG1FKSTCK1D1TWFPFDDORCEMKFGSWTYDGYOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA-----
                                                                                                                                                                                                                                                                                            cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furgs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDR 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: | |: | ||||||: || :|| || EEHHTAIGCNHKDLHLILKELQFITARMRKADDEAELIGDWKFAAMVVDR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%; Score 1253; DB 22; Length 498; illarity 50.4%; Pred. No. 1.4e-116; Conservative 53; Mismatches 108; Indels 102.
                                                                                                                                                                                                       Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
                                                   Myers EW;
                                                 Li PWD,
                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
267; Conserva
                                                                                  WPI; 2001-656860/75
              (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          498 AA;
                                                                                                    N-PSDB; ABL04535
                                                                                                                                                                          interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                  Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                        Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.8%; Score 1246; DB 15;
46.0%; Pred. No. 7.2e-116;
live 86; Mismatches 126;
                                                                                                                                                                                         /labe.
229..256
/label= TMD1
/.~+e= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                            /label= TMD4
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                        /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                    'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST BIOTECHNOLOGY IND ASSOC
                                                                                                                                                                                                                                                                                                                                                                                                                        /label= cytoplasmic_loop
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 80-81; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elliott KJ, Ellis SB, Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that express a variety of subtypes.
                                                                                                                                                                                                                                                                                                                                                 'note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SALK ) SALK INST BIOTECHNOLOGY (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                          1..23
/label= signal
                                                                                                                                                                                                                                                                                                      /label= TMD3
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.03
Matches 240; Conservative
                                                                                                                                                                                                                                                                                       290..317
                                                                                                                                                                                                                                                                                                                                                                                                           318..461
                                                                                                                                                                                                                                                                                                                                                                162..487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-303024/37.
N-PSDB; AAV12197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 AA;
                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9420617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1994;
                           14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                            Key
Peptide
                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                Domain
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126

62

186

AAW44153 standard; Protein; 502 AA.

RESULT 7 AAW44153

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123 191 183

131

63

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CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
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                                                                                                                                                                                                                                                                                                                                                                            SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                                                                                                                                                                                                                                                                                                                                    DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGGGDISSFVTNGEWELIGVPCKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SATTPPPAR-----VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                           Gaps
The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAC)R) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host recombinant alpha-7 subunit, opt. in combination with other recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                        70;
                                                                                                                                                                                                                                              Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFMVASSVVSTILLLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                           ; Score 1246; DB 18;
; Pred. No. 7.2e-116;
86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO2145 protein sequence SEQ ID NO:77
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.0%;
Matches 240; Conservative 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB24088 standard; Protein;
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                                                                                                                                                                                                   502 AA;
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                                                                                                                                      DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                   STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                 APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                           DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                              CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SATTPPPAR-------VPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORRCSLASVEMSAVAPPPASNGNILYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nicotinic acetylcholine receptor; nAChR; neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 MFMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW09025 standard; Protein; 502
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Water-soluble ligand-binding proteins derived from molluscs and analogues of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or schizophrenia -
                     CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                              -----SATTPPPAR-----VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                  361 ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                   393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
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Tyr210, Cys212, Cys213 and Tyr217 are
essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome;
                                                                                                               312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108...15
/note= "conserved ligand-binding region,
Trpl08 and Tyrl15 are essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                   SEAVCSEWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                             453 DADISRDWKFAAMVVDRLCLIFFTEFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trp171 and Tyr173 are essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotinic acetylcholine receptor alpha7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200158951-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOOMENTALAASLEHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTVYFSLSLLOIM
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                                                                                                                                                                                                                                                                                                                                                                                               Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.8%; Score 1246; DB 21; Length 51
46.0%; Pred. No. 7.2e-116;
Live 86; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Fig 58; 286pp; English.
                                                                                                                                                        99WO-US12252.
99US-0141037.
99US-0143048.
99US-0145698.
                                                                                                                                                                                                                                                       99WO-US28313.
                                                                                       2000WO-US00376
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                                                                                                                                                                                                                                                                                                                                                                                          Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                   Wood WI;
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                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-572270/53.
N-PSDB; AAC58395.
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WO200053755-A2
                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
                                                                                       36-JAN-2000;
                                                                                                                                                                                                                          26-JUL-1999;
30-NOV-1999;
20-DEC-1999;
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                                                                                                                                                                                                                                                                regions that are conserved throughout the various nach and which are essential for ligand binding. The invention relates to water soluble ligand-binding proteins derived from molluses, especially acetylcholine-binding proteins derived from molluses, especially acetylcholine-binding proteins derived from molluses, especially acetylcholine-binding proteins (AchBes) and analogues of ligand-gated ion channels, their crystals, and their cus for screening ligands of ligand-gated ion channels. The water-solubbe ligand-binding proteins are capable of forming multimers and are amenable to crystallization. The crystal models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-binding drugs that act con these con channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-benching solubility of the case the amino acids of the AchBe determining solubility of the came no acids of the AchBe determining solubility of the proteins, at least the essential amino acids of a ligand crops of the conserved regions of an naChB have been substituted for the conserved regions of an naChB have been substituted for the
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46.0%; Pred. No. 7.2e-116;
tive 86; Mismatches 126;
                                                                                                                                                                                                                                 nicotinic acetylcholine receptor (nAChR).
Disclosure; Page 252-254; 260pp; English.
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11 RESULT

The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see ARC90382 and AB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the DVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131 Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH ::|||:| ::| ||:|| ::| | |:|||||||:| ||: ||||| | |::|||||:| |:||||:| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:| : ||| :: ||||:|:||||||| ||:| E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIP 12 APAGLLLLCCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFPNLIVP CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI Gaps 70; Length 502; MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG--Indels Human; alpha7 nicotinic acetylcholine gated ion char 5-hydroxytryptamine; 5-HT3; calcium ion conductance. 46.8%; Score 1246; DB 22; 46.0%; Pred. No. 7.2e-116; iive 86; Mismatches 126; Wild-type human alpha7 ligand gated ion channel Disclosure; Pages 61-63; 77pp; English. MB: AA. Berkenpas (PHAA ) PHARMACIA & UPJOHN CO. 99US-0136174. AAB50012 standard; Protein; 25-MAY-2000; 2000WO-US11862. (first entry) Query Match
Best Local Similarity 46.0
Matches 240; Conservative Groppi VE, Wolfe ML, 2001-061524/07 502 AA; N-PSDB; AAC90380 WO200073431-A2. Homo sapiens. 27-MAY-1999; 14-MAR-2001 07-DEC-2000 AAB50012; Sequence 72 64 132 192 252 312 184 AAB50012 g g g ŏ g ò g ŏ ò δ ò

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                                                                                   Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;
immunochemistry; NAChR alpha? subunit; receptor.
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                                                                393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell comprising nucleic acids encoding human alpha and beta subunits neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -
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46.0%; Pred. No. 7.2e-116;
1ive 86; Mismatches 126;
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                                                                                                                                                                                                                        ABB82435 standard; Protein; 502
           ----SATTPPPAR--
                                                                                                                                                                                                                                                                                                         Human neuronal NAChR alpha7
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Monteggia

McKenna DG,

Gopalakrishnan M,

CA,

Briggs C Roch J,

(ABBO ) ABBOTT LAB.

96US-0771737

22-DEC-1997; 20-DEC-1996; <u>ы</u>

Touma

Sullivan JP,

WPI; 1998-377593/32 N-PSDB; AAV44687.

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the NAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR polypeptide.
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7.2e-116;
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46.0%; Pred. No. 7.2
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                                                                                                                                                                                                                                                                                                                                                                                                        alpha? nAChR activity or cytorotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating meurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha? the protein has about 1100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SPGGWMLALAASELHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                     Nucleic acid encoding variant of human alpha7 nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.6%; Score 1242; DB 19;
45.8%; Pred. No. 1.8e-115;
Live 86; Mismatches 127;
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: :    :  ::     :      :    :	QY 192 DEGGGDISSFVTNGEWELJGVPGKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLJVP 251 :	QY 252.CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311  Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300  QY 312 MFWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLXWLPWVLRMSRPGF 360  Db 301 MIT/GLSVVYTVLQYHHDDDGGRMPKMTRVILLNWGAMFLRMRRPGEDKVRPACOHK 360		QY. 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE 452	Qy 453 DADISRDWRFAAMVVDRLCLIFTLFTLATLAVLLSAPHIM 494 : :                 :	Search completed: August 13, 2003, 15:25:26 Job time : 44.5088 secs											
	QY 453 DADISRDKKFAANVUDRICLIFTLFTIATLAVLLSAPHIM 494  1 :	SULT 15 350015 AAB50015 stan AAB50015;	<pre>14-MAR-2001 (first entry) Mutant human alpha7 ligand gated ion channel #1.</pre>	<pre>KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant; KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein. XX OS Homo sapiens. OS Synthetic.</pre>		AX WO200073431-A2. XX YD 07-DEC-2000.	AA AA 25-MAY-2000; 2000WO-US11862. XX	PR 27-MAY-1999; 99US-0136174. XX	PA (PHAA) PHARMACIA & UPJOHN CO. XX	PI Groppi VE, Wolfe ML, Berkenpas MB; XX	DR WPI; 2001-061524/07. DR N-PSDB; AAC90385.	PT Special cell culture medium for treating cells and for inducing PT mammalian cell lines to conduct calcium ions, comprising specified PT concentrations of ions of sodium, calcium and potassium at specified pH	AA Claim 100; Pages 70-72; 77pp; English.	The present sequence is a mutant human alpha7 nicotinic acetylcholine cated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand cc gated ion channel (see AAC90382 and AB55014). The alpha7/5-HT3 chimeric cc ion channel can be expressed by recombinant cells in the present cc invention, resulting in preferential calcium ion conductance by the xx xx SQ Sequence 502 AA;	Ouery Match Best Local Similarity 45.8%; Pred. No. 2.9e-115; Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;	Qy 12 APAGLLLICLIWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71 :	Oy 72 DVDEKNOLLITNIWLKLEWNDMNLRNNTSDEGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131

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AK080415 Mus muscu AK029177 Mus muscu AI292581 GH15518.5 AK080475 Mus muscu AK049722 Mus muscu

AK080475 AK049722

AK034228 Mus muscu AK083157 Mus muscu BU149265 AGENCOURT AK051742 Mus muscu

AK081254 Mus muscu CB149460 K EST0205 BX403124 BX403124 BU91887 AGENCOURT BI516733 BB160023A BI516843 BB160023A CB245337 UT-M-FY0-AL058211 Drosophil BX477801 BX437801 AL064281 Drosophil 
AK051742 AK031228 AK031224 BU149265 AK081254 CEB4439460 BX4316643 BU5156873 BU516643 CCB24433 
AW914206 EST345510 AU120692 AU120692 BW717715 UT-E-CLI-BU702422 UT-M-FIO-BU161024 AGENCOURT BX421718 BX421718

AK087554 Mus muscu BQ720344 AGENCOURT CA374163 648474 NC BX299163 BX299163 AK041217 Mus muscu

BM711715 BUT02422 BUT02422 BUT01024 BX721718 AK087554 BQ720344 CA3749163 BX299163 AK041217 CA326954 CA326954 CA326954

CA326954 UI-M-FY0-BI195149 602944157 AL210044 Tetraodon AK030464 Mus muscu

AK010496 Mus muscu BE664308 148713 MA AL192274 Tetraodon

AK030464 AK010496 BE664308 CNS02DCP

ALIGNMENTS

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BG632919 885 bp mRNA linear EST 23-APR-2001 GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Sax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ Phydroidea: Drosophilidae; Drosophila.

[ Pases I to 885)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Contact: Stapleton, M.
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1101
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236.8
232.8
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213.8
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LOCUS
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JOURNAL
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AK053497 Mus muscu
AK051730 Mus muscu
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11127.831 Million cell updates/sec
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                                                                             August 21, 2003, 03:48:31 ; Search time 3249.96 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                              22781392 seqs, 12152238056 residues
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1488
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                                                    nucleic search, using sw model
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564; Conservative
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                                                                                                                                               /sex="male and female"
/dev.stage="adult"
/dab.bost="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/rolone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
Xhoi; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid CDNAs were directly ligated into a 205 c. 181 g. 242 t.
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          polyadenylated. The resulting Poly.T sequence has been removed. genomic AE003511: arm:X [18792641,1913647] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row: C column: 2
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this clone
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                                                                                                                                                                                                                                                                              Length 885;
more T residues at the beginning of the sequence,
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                                                                                             /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                            Score 476.2; DB 10;
Pred. No. 9.6e-110;
0; Mismatches 223;
                                                           High quality sequence stop: 784.
Location/Qualifiers
                                                                                                                                     /clone="GH16126"
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nilarity 73.2%;
Conservative 0
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Matches 6
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                                                    GGAACTIATITCAATIGCATIATGITATGIGGCCTCATCAGTIGIGGCCATACTI 106
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emboscope centre natural de Sequencaye
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
division of invitrogen..This sequence belongs to sequence cluster
Af46.r For more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq=CSODD07CH03QP1&cluster=7646.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODD007CH03QP1.
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
326 c 319 g 273 t 25 others
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| GGCACCTACTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTG
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                                                                                                                                                105 GTCCTCAATTATCATCATCATAAATCCAGATACGCATGAAATGAGTGAATGGGT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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AL530299 Homo sapiens NEGROBLASTOMA COT 50-NORM
CDNA clone CSODD007YP05 5-PRIME, MRNA sequence.
AL530299
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/mol_type="mRNA"
/db_xref="taxon:9606"
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g ò g õ g φ q ò q ò g ò qq ò qq ò Q ò Ω ò g ò Dp

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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishli,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Komo,H., Adachi,J., Fukuda,S.,
Alazawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bano,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Sarialand,T., Gissi,C., King,B., Kochiwa,H.,
Kuchl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Marchhonni,L., Mashim,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Bund, Hayshlzaki,Y.
                                                                                                                                                        Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsunato, H., Sakaguchi, S., Ikagami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, M., Ohara, E., Matshiki, M., Oraski, Y., Muramatsu, M., Inoue, Y., Tanaka, T., Matsuura, S., Kawai, J., Osakaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 (111-length cDNAs

Nature 420, 565-573 (2002)
6 (bases 1 to 1864)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
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Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Havi,F., Imotani,K., Ishii,Y., Itoh,W., Kagawa,T., Ksukawa,T.,
Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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Okazaki,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-ikahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muramatsu, and Hayashizaki, Y.

Direct Submission
Submitted (16-701-2001) Yoshinlade Hayashizaki, The Institute of Submission
Exploration Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (8-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
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Nature 409 (6821), 685-690 (2001)
21085660
prepare full-length cDNA libraries for rapid discovery of Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                      CGGCTCGTGTCTGTACGTGCCGCCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCAC 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                    CATCTGGCTAAAACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATGGCGAATGGGAGTTAATAGGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTG
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                                                                                                                                                                                                                                                                                                                      CTGGTTCCCCTTCGACGACCAACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGG
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                                                                                                                        CATTIGGCIGCAAAIGICITGGACAGAICACIATITACAGIGGAAIGICAGAAIAICC
                                                                                                                                                                               CGGGGTCAAAGATTTAAGAGTGCCACCCCACAGACTATGGAAACCAGACGTCCTTATGTA
                                                                                                                                                                                                                                                                                      907 TIGCICGCCACCTACTICAACTGCATCATGTICATGGTGG 946
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
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628 703 688 763 748 823 808 883 868

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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130068A06 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence. AKC51730.1 G1:26342155 HTC; CAP trapper. Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1004 TCACTATGATTTTTGTCACCTTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                             TCA----TTGGCTCCTCCATGAACCTCAAGGACTATTGGGAAAGTGGCGAGTGGGCCATCA
                                                                                                                                                                                                                                                                                                                                                                             GAGAAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGG
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                                                                                                                                                                               TGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCG
                                                                                                                                                                                                                                                                                                                                                                                               AAAACTGCACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGGTCC
                                                                                          TACAGGATGAAGGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAA
                                                                                                                                                                                                                                                                                                                             TGGCGGAGGACGATGCCAGCGACGTCGGACGCCCTGCCCTTGCTCGGCACCTACTTCAACT
                      AACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAAC
                                                                                                                                                                  TAGGAGTCCCCGCCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCG
                                                                                                                                                                                                                                    ACATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCG
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High-efficiency full-length cDNA cloning
Meth: Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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PFDYONCTWRFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
EEIYQOITYSLYIRRLDFYTINLIFCLLISSTTVLVFYLPSDGGEKYTLCISVLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHYRTPTTHTMPT
WKAAFLINCHENPRYRFSTBEDAFRTRNFYGELSALLGESKSCKEGYPCQ
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AQNYAKEJQDWKYYAMVIDRIFLWYFILVCTLGTAGLELQPLMARDDT"
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                                                                                                                                                                                                                                                            /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPIR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497) putative"
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     our web site for further details
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Pred. No. 2.8e-60;
0; Mismatches 469;
                                                                                                                                      /db_xref="FANTOM_DB:E130103E14"
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/clone="E130103E14"
                                                                                                                                                                                            /tissue_type="eyeball"
/clone_lib="RIKEN full-length
/dev_stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487
Please visit our web site for furt
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchl, P., Lewis, S., Matsuo, Y., Nikaido, I., Fresole, G., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, F., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Tyovooka, K., Schonbach, C., Seya, T., Shibata, Y., Stoch, K., Schonbach, S., Whittaker, C., Wilming, L., Wynshaw-Bozis, A., Yoshida, K., Wang, 
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Goroup Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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S Adachi,J., Alzawa,K., Akimura,T., Hara,A., Hashizume,W.,
Rukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayaksu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Ratoh,H., Kawali,J., Kojima,Y., Kondo,S., Konn,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Salito,R., Salito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinaqawa,A., Takaku-Akahira,S.,
Takeda,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
                                       Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIEB, Integrated sequence analysis (RISA) system--384-format Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
       Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
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URL:http://fantom.gsc.riken.go.jp/
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/strain="C57BL/6J"
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/protein_id="Bac34740.1"

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DGTGGYCHRERVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEA TÓSVKYIAENMK
AQNYAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
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EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
                                                                                                                                                /tissue_type="spinal ganglion"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TCA---TTGGCTCCTCCATGAACCTCAAGGACTATTGGGAAAGTGGCGAGGGGCCATCA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 TGCCCCCGCCGCTGTTGTCCATGCTGATGCTGGTGTTGATGCTGCTGCTGCTGCCAGTGGCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 GGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 GGAATGACTACAAGCTGAAATGGAAACCCTCTGACTACCAAGGGGTGGAGTTCATGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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db_xref="FanTOM_DB:D130068A06"
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Pred. No. 3.4
                                         /db_xref="taxon:10090"
/clone="D130068A06"
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrimi, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K., Suzuki, Y., Toyo-oka, K., Wang, K.H., Weitz, C., Whitteker, C., Willing, L., Waysshaw-Boris, A., Yoshida, K., Hassegawa, Y., Kawaji, H., Kohtsuki, S., Funchi, Lee, Marching, B., Khung, K., Ramaju, Y., Kawaji, H., Kohtsuki, S., Funchi, R., Shung, R., Khung, K., Khung, R., Khung, K.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas.

Nature 420, 563-573 (2002)

E (bases I to 3126)

Adachi,J., Aizawa,M., Akimuza,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,M., Hiraoka,T., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kaukawa,T., Katoh,H., Kawai,J., Kojina,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Muzata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakaume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sadaba,Y., Tanawa,P., Tawahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, WIRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site for further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="FANTOM_DB:A730007P14"
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152. .1666
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/clone="A730007P14"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
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PUBMED
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AUTHORS
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3126 bp mRNA linear HTC 05-DEC-2002
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:3473000/214 product:NEURONAL UCCTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikeqami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1080 TCACTATGATTTTTGTCACCTTGTCCATCGTCATCACAGGTCTTTGTGCTCAACGTGCACT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989 ACCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGC 1048
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                           929 GCATCATGTTCATGGTGGCTTCCTCCGTCGTCCTCACCATACTGATCCTCAACTACCACC
                                                                                                                                                                                                                                                                                                                                                                                                      900 ITCCGIGCTCATCTCCTTCCTCACTGIGCTCGTCTTCTACCTGCCCTCCGACTGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .020 TCACCGAGACCATCCTTCCACCTCACTGGTCATCCCTTGATCGGGGAGTACCTCCTT
                                                                                                          780 TTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAG
                                                                                                                                                                                  ACATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCG
                                                                                                                                                                                                                                                                                                                              749 TGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 GAGAAAAGTIGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGG
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                                     TAGGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCG
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GYPCODGTGCYCHHRFWISINSTRSSSSESVDAVLSLSALSPEIKEAIQSVKYI
AENMKAQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
                                                          /protein_id="Bac37909.1"
/db_xref="G1:26348539"
/db_xref="G1:26348539"
/ranslation="mrsSDMGYVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFED
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QGVEFNRVPARKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI
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Ltoh, M., Konno, H., Okazaki, Y., Muramatsu, M., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus 0 day neonate head cDNA, RIKEN full-length library, clone:4831406G09 product:cholinergic receptor, alpha polypeptide 1 (muscle), full insert sequence.

AK029177
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Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldacrili, R., Barsh, G., Blake, J., Boffelli, D., Bolunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchlonni, L., Mashima, J., Mazzarelli, J., Mombaerts, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)

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    /note="unnamed protein product; cholinergic receptor,
nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885,
GB|NM_007389, evidence: BLASTN, 99%, match=1763)

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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konto,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tamaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format
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GGCACGCTGCGGGTACCACGAGAAGCGGCTACTGCACCACTATTGGACCACTACAACGT 140
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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enriched library, clone:A730038F14 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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                                        112 AAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTTGCACCACCTACAATAC
                                                                                                          261 ACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGA
                                                                                                                                                                                                                                                                                                                                               TTTAAGAGTGCCACCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGA
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                                                                                   141 ACTGGAGAGCCCGTCGTCAACGAGAGCGACCGGTGCAGCTCTCCTTCGGCCTCACGCT
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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G15518.5518.5prime GH Drosophila melanogaster head port2 Drosophila melanogaster head port2 Drosophila melanogaster cDNA clone GH15518 5 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1; 04/10/2001, mRNA sequence.
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                                                                                                                                                                                                                                    965 CATCAACACACCACCGTTCGCCCAGCACCCACATCATGCCCGAGTGGGTGCGGAAGGT 1024
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/lab_host="DH5" - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
                                             915 CACCTACTICAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGAT 974
                                                                                                                              905 GAAGTATATGTTGTTCACCATGGTCTTTGTCATTGCGTCCATCATCATCACCGTCATCGT 964
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1 (bases 1 to 607)

1 (bases 1 to 607)

1 Arrey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Ewis, S. and Rubin, G. M.
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                    GTTCCTCAACATGGTGGCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003626; arm:2L [9617316,9882551]
estlimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
High quality sequence stop: 521
POLYA=No.
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
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68.5%; Pred. No. 2.1e-57;
tive 0; Mismatches 171;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Drosophila melanogaster
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/dev_stage="adult"
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Other_ESTs: GH15518.3prime
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.
Nature 420, 563-573 (2002)
6 (bases 1 to 2010)
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Nature 409 (6821), 685-690 (2001)
sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757–1771 (2000) 20530913
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Please visit our web site for further details
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   299
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167. 1673
/note="NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA SUBUNIT (SPTRIAAL58471, evidence: FASIY, 99.8%ID, 100%length, match=1497)
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                                                                                                                                                                                                                                                                  29 TGGCGCCCCCCCCCGCGGCCTGCTGCTGTGCCTGTTGCTCTGGCCGAGGGGGGCCACGCT
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Pred. No. 1.2e-55;
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TVEVLLISKYVPPTSLDVPLVGKYLMETWOLVTSIVTSVVLNVHHRSPTHTWAPW
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/dev_stage="12 days embryo"
200. .1705
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4037)
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GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
annotation of a full-length mouse cDNA collection (6821), 685-690 (2001)
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Please visit our web site for further details.
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Location/Qualifiers
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Best Local Similarity 51.5%;
Matches 709; Conservative
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Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530044Pi6 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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                                                                                                                                            987 CCACCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTG 1046
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             CTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAACTACCA
                                                                           1077 CTTCACTATGATTTTTGTCACCTTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCA
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ACCACGAGAAGCGGCTACTGCACCTATTGGACCACTACAACGTACTGGAGA 148			TCATCGACGTGGACGAGGAACCAGCTTTTAATAACAAACA	GGAATGATTGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG 328 		389 TCGACAGCACGTATCCAACGAACGTGGTGGTGCGAACAACGGCTCGTCTCTGTACGTGC 448	CGCCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACC 508 	AACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAAC 568 	TACAGGATGAAGGGGGGGGGAGTATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAA 628 	TAGGAGTCCCCGGCAAGCGCAACGAGTCTACTACAACTGTTGTCCGGAGCCATACATCG 688	ACATCACGITTGCGGTGGTGATCCGGAGGAAACGCTCTACTTCTTCAATCTGATCG 748 	TGCCCTGCGTGCTCATCGCCTCCATGGCTCTATGGGGTTCACCTTGCCTCCAGACTCCG 808	GAGAAAAGTIGICTITAGGIGIGGACGATATTACIGICGATGAGGGGGTGTTCCTCAACAIGG 868 	TGGCGGAGACGACGCGGCGGCGCGTGCCTTGCTCGGCACCTACTTCAACT 928 	GCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCCATACTGATCCTCAACTACCACC 988	ACCGCACCAGACACTCACGAAATGAGTGATTGGTTGCGTGTTCCTTTATTGGC 1048 	TGCCGTGGGTGCTGCGCTGCCGGCTCGGCGACGACGCCGCCGCCGGCGCGC 1108 	TACCTCCGCCGGACCTGGAGCTGCGGGGGCGCTCCTCCAAGTCGCTAGCGAACG 1168 
95 ACCACGAG			209 TCATCGAC        399 TCATCAGT	269 GGAATGAT			449 CGCCCGGC          639 CGCTGCC	509 AACGATGC   111 699 AGAACTGC	569 TACAGGAT       1 759 TCAAAAGC	629 TAGGAGTC 	689 ACATCACG          867 ACATCACC	749 TGCCCTGC          927 TCCCTGC	809 GAGAAAAG          987 GTGAAAAG	869 TGGCGGAGA         1047 TCTCCAAGA	929 GCATCATG         1107 TCACCATG	989 ACCGCCAC           1167 ACCGTTCG	1049 TGCCGTGG       1227 TGCCCACC	1109 TACCTCCG   1
ŏ ź			Qy 2 Db 3	Qy 2		Qy 3 Db 5	0y 4 Db 6	Oy 5 Db 6	Oy 5	8 . qq	9 Qy 0	Qy 7 Db 9	8 . da	Qy 8 Db 10	Qy 9	Qy 9 Db 11	Oy 10 Db 12	Qy · 11 Db 12

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SACCCATGTACCTGCTTTGTCAATCCTGCATGAATGCAGGGCTTGGCTGGGGCTT 1406
                                                                                                                                                                                                                                                                                                                            SAGCTCTCCCTCATTCTGAAGGAGATTAGAGTCATCACAGATCAGATGCGCAAGG 1348
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TGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCAATGCTGCCGAT 1228
                                                                                                                                                                AGGGGGGGGTGAGGAGAATGGCGGCGGGGTTGGCGGCGCACACTTGCTTCGGTGTCG 1288
                                                                                                                                                                                                          --- CTCCGGGAAGCTGTGGACGGTGTACGCTTCATTGCGGACCATATGCGAAGTG 1517
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H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
J. Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
J. Ishii,Y., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Ke,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
J.Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
Integrated sequence analysis (RISA) system--384-format
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Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Harabizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Ohno, M., Ohsato, N.,
Okazaki, Y., Zaito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomatu, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y. Oya, T., Yasunishi, A.,
Direct Submission
Submitted (16-JUG-2001) Yoshi, Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Styloration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,,
Fax. 61-75-803-9222,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sting, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., and Hayashizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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209. 1714
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KKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
HFPFDQQNCTMKFRSWTYDRTEIDLVLKSDVASLDDFTPSGEWDIIALPGRRNENPDD
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TVFLLLISKIVPPTSLDVPLVGKYLMFTMVLVTFSIVTSVCVLNVHHRSPTTHTMAPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKVVFLEKLPTLLFLQQPRHRCARQRLRLRRQREREGAGTLFFREGPAADPCTCFVN
                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.

Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDRAs

Nature 420, 563-573 (2002)

( bases I to 4046)

Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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AUTHORS
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JOURNAL
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640; Indels
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3.7e-54;
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0; Mismatches
                                                                                                                Score 258;
Pred. No. 3
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Best Local Similarity 51.5%;
Matches 709; Conservative
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gasterland,T., (Rissi,C., King,B., Kochiwa,H., Fleischmann,W., Gasterland,T., Rissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis S., Matsuo,Y., Nikaido,I., Rozuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bolinga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gestincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Narchhonni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Kingadd,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A. Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

Lu Nature 409 (6821), 685-690 (2001)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

L Nature 420, 563-573 (2002)

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E (bases 1 to 2940)

Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hirankot, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hirankot, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Miyazaki, M., Murata, M., Natana, M., Natana, M., Natana, K., Namazaki, R., Ohno, M., Ohato, M., Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Saatoh, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physical and Chemical Research (RIKEM), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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       Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; cholinergic recepnication; alpha polypeptide 4 (MGD|MG1:87888, GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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1049 TGCCGTGGGTGCTGCGCATGTCACGGCCCGGCTCGGCGACGACGCCGCCGCCGCCGCCGCCGC 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1416 TCCAGGCTGAGCCCGCTGCAGCCGGTCTGGGGCCCTCGATGGGCCCCATGCAGCTGTGGC- 1474
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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                                                                1236 TGCCCACCCTCCTCTTCCTGCAGCCACGCCACGCTGTGCACGTCAACGCCTGCGCT
                                                                                                                                   1109 TACCTCCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCTCCTAGCGAACG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630019M18 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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                                                                                                                 GACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGGGTG
                                                                                          ATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAACTACCACCACGGCACGCA
ATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATGTTC
                                             ATCCCGTCCACCTCGCTGGTCATCCCGCTCATCGGCGAGTACCTGCTCTTCACCATGATC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLAMFIIVCLLGTVGLFLPPW
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Radachi, J. Aizawa, K. Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Harandoto, K., Hiraokar, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kaqawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Shanazaki, R., Ohno, M., Oksacume, N., Sano, H., Sakati, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Saqabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomara, Y., Toya, T., Yasunishi, A., Kanishi, 
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VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFMIFVTLSIVITVFVLNVH
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanaqawa 230-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIESMHKMANAPRFWPEPES
EPGILGDICNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
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         Suzuki, H.,
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                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riken
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H. Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN
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nicotinic, alpha polypeptide 4 (MGD|MGI:87888,
GB|NW_015730, evidence: BLASTN, 99%, match=1946)
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Please visit our web site for further details.
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/clone_lib="RIKEN full-length
/dev_stage="adult"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCATGTTC 939
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakayuchi,S., Ikeqami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030030P04 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
    335 CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
                                                                                                                                                                                    GCACGTATCCAACGAACGTGGTGGTGCGGAACAACGGCTCGTGTCTGTACGTGCCGCCCG
                                                                                                                                                                                                                                                                          515 GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTACAGG
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                                                                     ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC
                                                                                                                                                                                                                                                                                                                                         GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAACGAT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                  AGENCOURT 8443358 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192234 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_l:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_l:
Directionally cloned using the following adaptors:
5'-TCGACCCAGGGGCCCG-3' and
5'-TCGACCCAGGGGCCCCCG-3' and
5'-GACTAGTTCTAGATCGGAGGGGCGCCCT(15)-3'. Size selected >
1'kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AGTICCAGAGGAAGCITTACAAGGAGCIGGICAAGAACTACAATCCCTIGGAGAGGCCCG 199
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                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to you, NIH-WGC http://mgc.nci.nih.gov/.NIH-WGC http://mgc.nci.nih.gov/.National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM13593 row
Plate: LLAM13593 row
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 908)
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens".
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6192234"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Robert Strausberg, Ph.D.
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, M., Ishai, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, Y., Okazaki, Y., Gojobori, T., Beno, H., Kasukawa, T., Saito, R.,
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Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H.,
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Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
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King, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Pynshav, Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Gases I to 3483)

E (bases 1 to 
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokohama,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/.URL:http://fantom.gsc.riken.go.jp/.Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="c57BL/6J"
/db_xref="FANTOM_DB:C030030P04"
/db_xref="taxon:10090"
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Direct Submission
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N
/tissue_type="corpus striatum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. 3483
/note="cholinergic receptor, nicotinic, beta polypeptide 2
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                                                               (neuronal) (MGD[MGI:87891, GB|NM_009602, evidence: BLASTN, 99%, match=1498)"
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                                                                                                                                                                                                                                                                                                               18; Gaps
                                                                                                                                                                                                                                                          Score 244.4; DB 11; Length 3483;
Pred. No. 9.8e-51;
); Mismatches 426; Indels 18;
                                                                                                                                                                                                                                                                                                            0; Mismatches
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429 CGGCTCGTGTCTGTACGTGCCGCCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCAC

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1 (bases 1 to 615)
Kim, N. S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
1048
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                                                                                                                                                                                                                                                                  1049 TGCCGTGGGTGCTGCGCATGTCACGGCCCGGC 1080
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Plate: 50 row: D column: 08
High quality sequence stop: 615.
Location/Qualifiers
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DB 14; Length 615;

Score 241.4; DB 14; Length Pred. No. 2.7e-50; 0; Mismatches 221; Indels

Query Match 16.2%; Best Local Similarity 63.1%; Matches 393; Conservative

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Mutant human alpha Mutant human alpha Mutant human alpha V274T variant huma Human polynucleoti

Human neuronal nic Human PRO2145 nucl

AAC58395 AAC90385

AAC90386

AAC90387 AAV44687

Human neuronal NAC

Neuronal nicotinic prostate cancer-as Drosophila melanog Neuronal nicotinic Chimeric alpha7/5-Human mutant neuro DNA encoding novel

Human neuronal nic Human neuronal nic

Alpha4 subunit of Human neuronal NA

AAT48235 ABK92165 ABK92165 AAT48236 AAT48236 AAD26345 AAD26345 AAS95527 AAT59527 ABV73244 ABV73244 ABS54871 ABS54871

Human CHRNB2 codin

Human neuronal nic Neuronal nicotinic Human neuronal NAC Human neuronal nic

AAV12201 AAV48240 ABV73249 ABS54876 AAT59528

AAT48237 AAQ14288 AAN50416

AAL45873 AAZ38821

Alpha 2 subunit of Human neuronal NAC Human neuronal nic

Neuronal alpha-bun Neuronal alpha-bun Human neuronal nic

AAT59196 AAT59197

AAV12199

AAQ90387

ABV73243 ABS54870

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
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"/tbg" a
/product= "acetyl-choline receptor"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                       This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Hellothus virescens.
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                                                      New nucleic acid encoding a nicotinic acetylcholine receptor insects, used to identify potential insecticides \,
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1488; Conservative 0; Mismatches
                                                                                                 Claim la; Page 14-17; 26pp; German
              2000-014207/02
                             PSDB; AAY50815
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                                                                                                                                                                        TTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTGGCGGAG
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Pred. No. 3.7e-130;
0; Mismatches 460;
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Local Similarity 64.6%;
Les 929; Conservative
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                                                                                                                 GGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel nucleic acid (Nh) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, lits regulatory regions, and antibodies directed against (1) encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to recombinant production of (11). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTA
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                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding a nicotinic acetylcholine receptor insects, used to identify potential insecticides
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                                                                  "acetyl choline receptor.
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0; Mismatches 502;
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               Location/Qualifiers
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P-PSDB; AAY50814.
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878; Conserv
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570 585 630 645 690 705 750 765 810 825 870 885

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
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 CGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTA
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176 ABL30511), expressed DNA sequences (ABL016176 ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGTCGTCAACGAGGGACCCGCTGCAGCTCTCCTTCGGCCTCACGCTCATGCAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681
                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                   PWD,
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Best Local Similarity 72.9%;
Matches 605; Conservative
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11-JUL-2000; 2000US-0614150
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                                                                              pharmaceutical; gene; ss
                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                  Venter .JC, Adams M,
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P-PSDB; ABB69630.
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26-MAR-2002
                                                            Drosophila;
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1192 GGGTCGACCCGGTCGCAAGATTACACGCAAAACAATACTATTAAGCAATCGCATGAAGGA 1251
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   1372 TCGGCCCACACACGGTGGAGGAGCATCACACGGCCATCGGCTGCAATCACAAAGATCTTCA
                                                                                              948 TTCCTCCGTCGTCTCCACCATACTGATCCTCAACTACCACCGGCACGCAGACACTCA
                                                                                                                                                                                          1008 CGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGGGTGCTGCGCAT
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5-hydroxytryptamine; 5-HT3; calcium ion conductance;
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    and
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                                                                                                                                                                                                                                                                                          412 TGAGGGATTCGATGCCACGTATCACACCAACATTGTGGTCAAACATAACGGCAGTTGTCT
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                                                                                                                                                                 Gaps
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7777-ABR2072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                        Score 458.2; DB 23; Length 1540;
Pred. No. 9e-102;
0; Mismatches 493; Indels 99;
                                                                                                                 Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 other;
                                                                                                                                       7 Match 30.8%;
Local Similarity 60.1%;
hes 893; Conservative
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                                           ЬH
                                                                                                            The present sequence is the coding sequence for wild-type human alpha7 nitochinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptemine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
                                                                                                                                                                                                                                                                                                                 CGCCCGCGGCCTGCTGCTGCTGCTGCTTGCCTGGCCGAGGGGGGGCACGCTGCGGGT
                                                                                                                                                                                                                                                                                                                                              CGCCGGGAGGCGTCTGGCTGGCCGCTCGCTCCTGCACGTGTCCCTGCAAGGCG
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           Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                       Score 405.6; DB 22; Length 1509;
Pred. No. 6.1e-89;
0; Mismatches 604; Indels 42;
                                                                                                                                                                                                                              Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                  Example 5; Pages 60-61; 77pp; English
                                                                                                                                                                                                                                                         27.3%;
56.5%;
                                                                                                                                                                                                                                                                                   840; Conservative
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Best Local S:
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ligand-gated receptor; ds.
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                                                                                                                                                                                                                                                  the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammallan cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAV48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that
                                                                                                                                                            Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                      sequence (AAT48239) codes for the alpha-7 subunit (AAW09025)
                                                                                                                                                                                                                                                                                                                                                                                Score 405.6; DB 18; Length 1876;
Pred. No. 6.5e-89;
0; Mismatches 604; Indels 42:
                                                                                                                                                                                                                                                                                                                                                         Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
                                                                                                                                                                                                       Disclosure; Page 71-73; 108pp; English.
                                                                                                                                                                                                                                                                                                                            modulate the activity of human nAChRs.
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Best Local Similarity 56.5%;
Matches 840; Conservative
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96WO-US09775
                             95US-0484722
                                                                                      Elliott KJ, Harpold MM;
                                                                                                                WPI; 1997-065463/06.
P-PSDB; AAW09025.
07-JUN-1996;
                             07-JUN-1995;
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                               443 CCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACCTGCCTCCAG
                                                              GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAACGAT
                                                                              GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTACAGG
                                                                                                                                                                                 ATGAAGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta MachRs Bubunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and design of individual subunits and should lead to the identification and design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGGGCCCG
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                                             "neuronal nicotinic acetylcholine receptor alpha-7 subunit"
                                                                                                                                                                                                                                                                                                                              Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 1876;
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Pred. No. 8.2e-89;
1; Mismatches 604;
                                                                                                                                                                                                          (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (SIBI-) SIBIA NEUROSCIENCES INC.
Location/Qualifiers 73..1581 /*tag= a /product= "neuronal n
                                                                                                                                                                                                                                                        Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 78-79; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that express a variety of subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 27.2%;
al Similarity 56.5%;
839; Conservative
                                                                                                                                                  94WO-US02447
                                                                                                                                                                             93US-0028031
                                                                                                                                                                                                                                                                                                                                                             activity of the receptor
                                                                                                                                                                                                                                                        Elliott KJ, Ellis SB,
                                                                                                                                                                                                                                                                                    WPI; 1994-303024/37.
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                                                                                         183 ATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGCGCTTTGACG
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              TCGTCAACGAGAGCGACCCGCTGCAGCTCTCCGCCCTCACGCTCATGCAGATCATCG
                                                                          ACGTGGACGAGAAACCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGTGGAATG
                                                                                                                                                                                                CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
                                                                                                                                                                                                                                                            395 GCACGTATCCAACGAACGTGGTGCTGCGGAACAACGGCTCGTGTTCTGTACGTGCCGCCCG
                                                                                                                                                                                                                                                                            GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha7 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 CGCCGGGAGGCGTCTGGCTGGCGCTGGCGGCTCTCCTGCACGTGTCCCTGCAAGGCG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCACGAGAAGCGGCTACTGCACCACTATTGGACCACTACAACGTACTGGAGGGCCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;
immunochemistry; NAChR alpha? subunit; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell comprising nucleic acids encoding human alpha and beta subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elliott KJ;
                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "NAChR alpha7 subunit"
/note= "neuronal nicotinic acetylcholine receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans
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                                                                                                                                                                                   neuronal NAChR alpha7 subunit encoding cDNA
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Pred. No. 8.2e-89;
1; Mismatches 604
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73..1581
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                                                                                       ABV73248 standard; cDNA; 1876
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                                                                                                                                                                                                                                                              Homo sapiens
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CCTTCACAGTGACCATGCGCCGCAGGACGCTCTACTATGGCCTCAACCTGCTGATCCCCT 793
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 nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                          335 CCCACAGAGCTATGGAAACCAGACGTCCTTATGTACAACAGCGGGGGGGCGAGGGTTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 ACCACGAGAAGCGGCTACTGCACCACTATTGGACCACTACAACGTACTGGAGAGGCCCG
                                                                                                                                                                                                                                                                       263 ACGTGGATGAGAACAACTTTTAACCACCAACATTTGGCTGCAAATGTCTTGGACAG
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                                                                                   DB 24; Length 1876;
                                                                                                             1; Mismatches 604; Indels
                                                      Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
                                                                                   Score 405.2; DB 2
Pred. No. 8.2e-89;
                                                                                   27.2%;
                                                                                                             Matches 839; Conservative
                                                                                                 Similarity
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                                                                          GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGCGACTGGA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for identifying compounds that are matagonists or agonists of human neuronal nicotinic acctylcholine receptors (nNAChRs). By contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an
                                                                                                                                                                    AGTICGCCGCCATGGTCGTGGACAGACTGTGCCTTATTATCTTTACCCTGTTCACAATCA
                                                        ---ATTCTGAAGGAGATTA
                          Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NNACDR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neuronal nicotinic acetylcholine receptor; nNAChR; gene; ion flux; alpha 7 subunit.
                                                                                                                                                                                                                                           TCGCCACGCTAGCCGTGCTGTCCGCGCCACACATCATGGTGTC 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Human nNAChR alpha 7 subunit"
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73..1581
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                                                      TCGACTACGAGCTCTCCCTC---
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92US-0938154.
93US-0028031.
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08-MAR-1993;
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Baker KP,
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         (GETH ) GENENTECH INC.
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                             Ashkenazi AJ,
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                                                  GGGTGCTGCGCCATGTCACGGCCCCGGCTCGGCGACGACGCCGCCGCCGCGGCGCGCGTACCTC
                                                                      GGTTCCTSCGAATGAAGAGGCCCGGGGAGGACAAGGTGCGCCCGGCCTGCCAGCACAAGC
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                                                                                             1115 CGCCG------CCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCTCCTAGCGA
                                                                                                                                       ACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCGCAGCGCAATGCTGCC
                                                                                                                                                   GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGGCGACTGGA
         <u> ACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGT</u>
                                                                                                                                                                                                                                                                                                                                                                      TCGCCACGCTAGCCGTGCTGCTGTCCGCGCCCACATCATGGTGTC 1487
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05-JAN-2000;
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0290, PR0311, PR0535, PR0619, PR06119, PR0717, PR0819, PR0814, PR04318, PR04105, PR01103, PR01103, PR01103, PR01103, PR01101, PR01101, PR01103, PR01103, PR01104, PR01104, PR01104, PR01104, PR01104, PR01104, PR01104, PR01104, PR01104, PR02108, PR02108, PR03108, PR03104, PR
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                                                                                                                                                 PRO polypeptides, useful in the of cancer -
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0; Mismatches
                                                                                                                                                       Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                         Claim 50; Fig 57; 286pp; English.
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Matches 839; Conservative
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                                           ATGAAGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGGTAATAGGAG
                                                                                                                                                                                                                                                   TGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAACTACCACCACGGC
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                                                                                   GCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGAGAAA
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                                                                                                              TCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGACATCA
                                                                                                                                                       CGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTGCCCT
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95 ACCACGAGAAGCGGCTACTGCACCACTATTGGACCACTACAACGTACTGGAGAGGCCCG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 CCCCCCCCCCCCTCCTCCTCTCTCTCTCTCCCCCAGGGGGCCACGCTGCCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                            Mutant human alpha7 ligand gated ion channel coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1509;
                                                                                                                                           Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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56.5%; Pred. No. 1.5e-88;
ive 0; Mismatches 605;
                                                                                                                                                                                                                                                                                                                                                                               MB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 50; Page 69; 77pp; English.
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Matches 839; Conserv
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                                       A------GGCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGACCTAGTGGGAA
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                                                                GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACGAT
                                                                            GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytrypteamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 20 substituted by a proline residue and the wild-type cysteine residue at position 241 substituted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 CGCCCGCGGGCCTGCTGCTGCTGTGCCTGCTCTGGCCGAGGGGGGCACGCTGCGGGT
                                                                                                                                                                                                                                                                                                                     mutant;
                                                                                                                                                                                                                                        coding sequence #3.
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Pred. No. 3.7e-88;
0; Mismatches 606; Indels 42;
                                                                                                                                                                                                                                                                                                             Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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1226 GATACTACAGGGGGGGGGGGAAATGGCGGGGGTTGGCGGCGCACAGTTGCTTCGGTG
                                                                                                               1262 TGCACGGCGGGCAACCCCCCGAGGGGGACCCGGACTTGGCCAAGATCCTGGAGGAGGTCC
                                                                                                                                         GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGCGACTGGA
                                                                                                                                                                GCTACATTGCCAATCGCTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGCGAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; canconeurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease; schizophrenia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding variant of human alpha7 nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
                                                                                                                                                                                                                                                         1442 TCTGCACCATCGGCATCCTGATGTCGGCTCCCAACTTCGTGGAGGC 1487
                                                                                                                                                                                                                                           TCGCCACGCTAGCCGTGCTGTCCGCGCCCACATCATGGTGTC 1487
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                                                                                       1286 TCGACTACGAGCTCTCCTC-
                                                                                                                                                                                                                                                                                                                                 AAV44687 standard; cDNA; 1590
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livan JP, Touma E
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dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in sttu immuno-fluorescent assay). Compared with wild-type alpha? nAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (incotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
and immune
     affective disorders
enzyme dysfunction,
neurodegeneration,
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Sequence 1590 BP; 322 A; 471 C; 449 G; 348 T; 0 other;

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Score 394; DB 19; Length 1590;
Pred. No. 4.2e-86;
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time : 405 secs Job THIS PAGE BLANK (USPTO)

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 21, 2003, 00:04:15; Search time 5546.39 Seconds (without alignments) 10975.350 Million cell updates/sec US-09-303-232-3\_copy\_335\_1822 1488 1 atgggcgggcggcgccg.......cgccacacatcatggtgtcg 1488 5777422 Total number of hits satisfying chosen parameters: 2888711 seqs, 20454813386 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapov 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 em\_vi:\* em\_htg\_hum:\* gb\_vi:\* em\_ba:\* em\_fun:\* gb\_ro:\* gb\_sts:\* em\_hum:\* em\_ro:\* em\_sts:' : gb\_ba:\* : gb\_htg:\* em\_ov:\* em\_pat: em\_un:\* gb\_in:\* gb\_om:\* gb\_ov:\* gb\_un : 1 em\_in:\* em\_mu: em\_or:' em\_om: GenEmbl:\* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

em\_htg\_mam:\*
em\_htg\_vrt:\*
em\_sy:\*
em\_htgo\_hum:\*
em\_htgo\_mus:\*
em\_htgo\_other:\*

em\_htg\_rod:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result  10  11  12  3  3  4  6  6  6  6  6  6  6  6  6  6  6  6
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Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
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0; Mismatches 0;
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                                                                          and Adamczewski, M.
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Schulte, T., Oellers, N. and Adamcze
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Be
51368, Germany
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Nucleic acid encoding insect actyl ch E58347

E58347.1 GI:13019346
JP 2000023680-A/2.
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IDDDFRHPQAQOPQCRYTRGGEBNAAGLAAHSCFGVDYELSLILKEIRVITDQMRKD
DEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS"
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                        Pterygota
                                                                  Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.
Wotleic acids encoding acetylcholin-receptor subunits from
Patent: EP 0962528-A 3 08-DEC-1999;
BAYER AG (DE)
                                   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysiā;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dit
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ilarity 100.0%; Pred. No. 6.4e-291;
Conservative 0; Mismatches 0;
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/wol_type="genomic DNA"
/db_xref="taxon:7102"
335. 1825
/note="unamed protein product"
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Drosophila melanogaster
Eukaryota; Metazao; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Glossata; Ditrysia; Noctuoidae; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3701)

5 Martin, A., Nadja, E. and Thomas. S.
Nucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 2 25-JAN-2000;

BAYER AG

OS Heliothis virescens
PD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAX-1998 DE 19819829.9
PR 04-MAX-1998 DE 19819829.9
PR 04-MAX-1999 DE 19871847705,CO7K16/28,CI2NIS/10, PC C12NIS/09,A01K67/033,CO7K14/705,CO7K16/28,CI2NIS/10, PC C120X/68,
PC G01N33/15,G01N33/50//(C12NIZ/21,C12R1:19),C12NIS/00
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
/db_sref="taxon:7102"
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Location/Qualifiers
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100.0%; Pred. No. 6.4
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CCCGCTGCCAGCGTCGCTGTCGCTGTTGTCCTTGATCTTCTGGCGATAATTAAAGA 446
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                                                                                                                                                                                               81 GGCACGCTGCGGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGT
                                                                                                                                                                                                                   AAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTCACCTACAATAC
                                                                                                                                                                                                                                                                                    ACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGGAGTGGAACGACTACAATCTGCGCTGGAATGAAACGGAATACGGCGGGGTCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ACTGGAGAGGCCCGTCGTCAACGAGAGCGACCCGCTGCAGCTCTCCTTCGGCCTCACGCT
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                                                                          3.4e-114;
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No. 3
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/protein_id="AAM13393.1"
/protein_id="AAM13393.1"
/bc.xref="G1:20152847"
/translation="MDSPHPASLSLEVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTLERPVANESEPLEWREGLTLQQIIDVDEKNQLLITNLALSLEWNDYNLRWNETEYGGW
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHGGSCLYVPPGIFKSTCKMDITW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLTVFLNLVAESMPTTSDAVPLIGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEM 
PPWHKSVFLOWLPWILRMERGERKITRKIILLSHWRKELELEKERSSKSILANVLDIDD 
DFBHTSOSGOQFASSASFGRPTTVEEHHTALGCNHKDLHIILKELQFITARMRKADD 
EAELIGDWKFAAMVUDRFCLIVFTLFTIIATVTVLLSAPHIIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDF1TNGEWYLLAMPGKKNT1VYA
CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compared
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="results in glycine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626 and in variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor; alternatively spliced; contains exons 3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ion channel; neurotransmitter transmembrane
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                                                                                                                                                                                                                                                                                                                    melanogaster'
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/replace="t"
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to variant clone"
                                                                                                                                                                                                                                                                                               1. .2023
/organism="prosophila me/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="nAcRalpha-30D"
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1. .2023
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                       2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
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CCPEPYVDITFTIQIRRRTLYYFRNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVPLNLVABEMPTTSDAVPLIGTYFNCINFWASSVVLTVVVLNHHRTADIHEM
PUNKSVFLQMLPWILMRGFGKKTRYTILLSNRMEELELKERSSKSLLAWUDIDD
PPRHTISGSQTAIGSSASFGRPTTVEBHHTAIGCNHKDLHLILKELQFITARMRKADD
                                                                                                                                                                                                                                                                                                       TITAATIGIGCCATGTGCTAATCTCATCGATGCCCCTACTGGGCTTCACATTGCCGCC
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                                                                 EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ
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                                                                                                                    /gene="nAcRalpha-30D"
/product="nicotinic acetylcholine
Dalpha6"
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Pred. No. 1.5e-113;
0; Mismatches 517;
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/gene="nAcRalpha-30D"
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ERPVANESEPELWKFGLTLQQIIDVDEKNQLLITNLMISLEWNDYNLEWNFFFKGGWK
DLRIPNKLWRPDVLMXVRGEGDGTYTTSVVVKGSCLYVPPGIFKSTCKMDITW
FPFDOPLCEMKFGSPTTYDGNQLDLVLSSEDGGDLSDFITNGEWYLLAMPGKKTIVYA
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                                                                                                                  ATGCTGCCGATACTACAGGGGGGGGGTGAGGAGAATGGCGCGGGGGTTGGCGGCGCCACAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATGGCTGCCCTGGATCTTGCGAATGGGTCGACCCGGTCGCAAGATTACACGCAAAAC
                                                                                                                                                               CCTAGCGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCGCAGCCGCA
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                                    TTATTGGCTGCCGTGGGTGCTGCGCATGTCACGGCCCGGCTCGGCGACGACGCCGCCGCC
                                                                                                  GGCGCGCGTA---CCTCCGCCGCCGGACCTGGAGCTGCGCGAGCGCCTCCTCCTAAGTCGCT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1665)
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Dalpha6"
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University College London, Gower Street, London,
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/db_xref="G1:29466435"
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44. .1528
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South Park Road, Oxford OX1
                                                           melanogaster"
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Wismatches 517;
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Genetics Unit, University of Oxford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="results in glycine to the sequence deposited AE003626"
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                                                                                                                                                                                                                                                               variant type III"
/protein_id="AAM13394.1"
/db_xref="G1:20152849"
                                                       /organism="Drosophila
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                          /gene="nAcRalpha-30D"
379. .1863
                                                                                                                                                                                      /gene="nAcRalpha-30D"
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                                                                                                                                /dev_stage="embryo"
1. .2023
                             Location/Qualifiers
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ilarity 64.4%;
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                                                                       980
                           Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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                                                                                                                                                                                                        CAACATGGTGGCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTA
                                                                    CTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAA
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
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Drosophila melanogaster
Busaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Grauso, M. and Sattelle, D.B.
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CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTLL
LSLTYVELNAFTLEQVSDA.PELGTYFNCINFWASSVVLTLYVVLLWYHHRTADIHEM
PPWIKSVFLOWLPWILMBORGKTITKTILLSNRWKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTATGCNHKDLHLILKELQFITARNRKADD
EAELIGDWKFAAMVVDRFCLIVFTLFIIATVTVLLSAPHIIVQ"
                                                                                                                                                                             /translation="MDSPLPASLSLEVLLIFLATIKESCOGPHEKRLLNHLLSTYNTL
ERPVANESEPLEVKFGLTLQOIIDVDEKNQLLITNLMLSLEMNDYNLRMNETEYGGVK
DLRITPNKLMKPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKMDITW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GCCACGCTGCGGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGT
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in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
/note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b
                                                                        /product="nicotinic acetylcholine receptor Dalpha6
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INV 29-APR-2002

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/profein_id="AaM13392.1"
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/db_xref="G1:20152845"
/fb_xref="G1:20152845"
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CCPEPYVDTTFTIQIRRRTLYYFFNLLYPCVLLSSMALLGFTLPDSGERLTLGVTLL
CZETVPCLNLYAETLPQVSDAIPLLGFYPNCIMFWVASSVVLTVVLNYHHRTADIHEM
PPWIKSVFLQMLPWILLAMGREGRKTPRKTILLSNRKFELELERERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELOFTTARMKEDD
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                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2023)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Davel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
Genetics 160 (4), 1519-1533 (2002)
21969411
11973307
                                                                                 Arbana linear INV 29-APR-20 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type I (nAcRalpha-30D) mRNA, complete cds, abranalively spliced.
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/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="results in asparagine to glycine substitution; compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a
                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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 GGTGCTCTCCGCTCCGCACATAATCGTG 1857
                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/cbromosome="2"
/map="30b1"
/dev_stage="embryo"
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Grauso, M. and Sattelle, D.B.
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CGAAGGGTTCGACACGTATCCAACGAACGTGGTGGTGCGGAACAACGCCTCGTGTCT
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Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
                                                                                                                                                                                                                                                                                                                                                                                               AATACTATTAAGCAATCGCATGAAGGAGCTGGAGCTAAAGGAGGCTCCTCCAAAATCCT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="results in asparagine to serine substitution;
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/note="compared to variant clone"
/replace="t"
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                                                                                                                                                                                                                                                                                                    Score 608.6; DB 3;
Pred. No. 6.7e-113;
0; Mismatches 519;
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                                             /gene="nAcRalpha-30D"
/note="compared to variant
/replace="a"
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/note="compared to variant
/replace="t"
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/gene="nAcRalpha-30D"
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                                     to serine substitution;
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                                                                                                                                                     Length 2907;
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                                                                                                                                                 Score 583.8; DB 3;
Pred. No. 7.1e-108;
); Mismatches 422;
                                     /note="results in asparagine
compared to B allele"
/replace="9"
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                     /gene="nAcRalpha-34E"
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IWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRC
EMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPFPYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"mknaqlkltevdddelwlavrlahcssnfsssstrttssnqrh
nqqlttlqprslstkhhsnlaseqhnsqqqepaskdedvanhgrsndqqthlqqldss
nmlspktaaaataagdeattqqptnlrlcarkrqrlrrrrrrrrpatpretdlkkqqql
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NNSSTQILNGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNES
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EYELGLILKEIRFITDQLRKDDECNDIANDWRFAAMVVDRLCLIIFTMFAILATIAVL
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/note="results in threonine to isoleucine substitution;
compared to B allele"
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/note="results in deletion of asparagine and serine;
/ronjared to B allele"
                                                                    To bases 1 to 2907)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford Oxl 3Qx, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     'note="ion channel; neurotransmitter transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nicotinic acetylcholine receptor Dalpha5
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/note="results in serine, glycine, and asparagine
insertion; compared to B allele"
/replace="agoggcaac"
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/note="results in phenylalanine to isoleucine
substitution; compared to B allele"
                                                                                                                                                                                                          /organism="Drosophila melanogaster"
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/note="compared to B allele"
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
21969411
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compared to B allele"
/replace="gg"
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1. .2907
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PPNSTASTGNLGPGCSIFRTDFRRSTYRPSTWEDVGGLGSHHRELHILLRELQFITA
'product-"putative nicotinic acetylcholine receptor alpha
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Schulte, T., Oellers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Cell
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CCATGGATATTGCGAATGAGTCGCCCAGGACGACGCTGATCCTAGAGTTCCCGACCACG
                                                                                                     --CCGGACCTGGAGCTGCGC
                                                                                                                   GAGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCTCGACGATGACGACTTCCGCCAC
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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95. 1600
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                                          CCGTGGGTGCTGCGCATGTCACGGCCCGG
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/note="hvnachra7-2"
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Schulte,T., Oellers,N.
Direct Submission
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CDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYV
DVTFTIMIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFL
                                           NLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSV
FLQWLPWILRMSRPGKKITRKTIMMWTRMRELELKERSSKSLLANVLDIDDDRFHGPP
PPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGLGSHHRELHLILRELQFITA
RMKADDEFAELISDWKFAWVVDRFCLFVFTLFTIIATVAVLLSAPHIIVQ"
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/translation="MAPMALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANE
SEPLEVRRGGTILQJIIDVDERNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPN
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ORIGIN  Query Match  38.6%; Score 575; DB 6; Length 3109;  Best Local Similarity 64.6%; Pred. No. 4.3e-106;  Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;  Qy 97 CACGAGAAGCGCTACTGCACCACTATGGACCACTACAAGGACGCCCTC 156	217 GTGGACGAGAACCAGGTTTTAATAACAAACATCTGGCTAAAACTAGAGTGGAATGAT [	458 ACCTACCAGACCAGGGGGGGGGGGGGGGGGGGGGGGGGG	637 CCGGGAAGAGGAATCTACTACTACGTTGTCCGGAGCCTACATCATCACG  1   1   1   1   1   1   1   1   1   1	Db   878   CTCACACTTGGAGTCACTATTCTTTTTTTTTTTTTTTTT
997 GCAGACACTCACGAAATGAGTGATTGGATTGCTTGCCTTTATTGGCTGCCGTGG 11	Qy         1174 GACATCGACGCACCGCAAGCGCAACCGCAATGCTGCG 1226           Db         1238 GATATTGATGATGACTTCAGACACGCCTCCGTACAGTACTGCTCGACCGG 1297           Qy         1227 ATACTACAGGGGGGGAGGAATGCCGCCCCCTCACAGTTGCTCGCTC	Qy         1369 TGGGGGAGTTGGCGCCATGGTGGGACAGACTGTGCCTTATTATCTTTACC 1428           Db         1478 ATCAGGGAGTTGCTGGGATGGTTGTTGATAGGTTTTGCTGTGTTCACA 1537           Qy         1429 CTGTTCACAATCATCGCGACGGTAGCTGTTGCTGCTGCCGCCACACATGATGGTG 1485           I         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TON Nucleic acid encoding insect actyl choline receptor subunives 58348  S 48138.1 GI:13019347  S 4P 2000023680-A/3.  Hellothis virescens (tobacco budworm)  ISM Hellothis virescens (tobacco budworm)  ISM Hellothis virescens (tobacco budworm)  ISM Hellothis virescens (tobacco budworm)  Redaryota Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuoidea; Hellothinae; Hellothis.  I (bases 1 to 3109)  RS Martin,A., Nadja,E. and Thomas,S.  Nucleic acid encoding insect actyl choline receptor subuni and the Patent: JP 2000023680-A 3 25-JAN-2000;	December   December

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                                                                               /product="nicotinic acetylcholine receptor subunit
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VDRLCLIIFTLFTIIATLAVLFSAPHFIVSGVRG"
                                                                                                                                                          Score 568.4; DB 3;
Pred. No. 9.1e-105;
0; Mismatches 416;
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/gene="nAcRalpha-18C"
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NSSEFGCYNDLAIPPHILMKPDYLAWNSADEGFDGTYATNVVVRNNGSCLYVPPGIFK
STCTITTWFPFDDQRCEMFGSWTYDGFOLDLQLODBGGGDISSFITNGEWDLLGVP
GKRNELYYNCCPEPY TOITFALLIRRYLLYFFNLLYPCVLLASMALLGFTLPDSGE
KLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGKYENCIMEMVASSVVSTILVLNYH
HRNDPTHEMSEWIRVIFLYMLCILLMKORPGVGYEDEPPSSSSSSASGEKKQIQN
VELKERSSKSLLANLDIDDDFCKNHRCASATLPHQPTYRFTWYRQCDDGSVGPVGP
GPVVDGRLHEAISHTCLISSAEYELALLKELRWITEQLKKEDETSDITRDWKFAAMV
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/translation="MSFPQPHSLPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH
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Drosophila melanogaster mRNA for nicotinic acetylcholine receptor
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                                                                               GACATCGATGACGACTTCCGCCACCCGCAAGCGCAGC
                                                                                                                                                                             -----GTGTCGACTACGAGCTCTCCCTCATT
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                             ATACTACAGGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCACAGTTGCTTCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="nicotinic acetylcholine receptor
Dalpha7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-MAR-2003) Millar N.S., Department o
University College London, Gower Street, London,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nAcRalpha-18C gene; nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit Dalpha7 (nAcRalpha-18C gene)
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26. .1654
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/db_xref="taxon:7227"
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AJ554210.1 GI:29466436
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Millar, N.S.
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DME554210
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/product="nicotinic acetylcholine receptor Dalpha6 subunit variant type IV"

variant type IV"

/db.aref="G152851"
/db.xref="G152851"
/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWVASSVVLTV
VVLNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSSKSLLANVLDIDDDFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLIL
KELQFITARWRKADDEAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERPVANESEPLEVKFGLTLQQ1IDVDEKNQILTTNAMLNLDEKNQLLITNLWLSLEWN
DYNLRWNETEYGGVKDLRITPNKLMKPDVLMYNSADEGFDGTYHTNIVVKRSGSCLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="results in methionine to isoleucine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="nAcRalpha-30D"
//note="results in arginine to histidine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="results in serine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                    /note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 3b
8b; contains two repeats of the functional domain loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGCACTTGGCGGCGCCCGCGGGCCTGCTGCTGCTGTGCCTGCTCTTGGCCGAGGGG
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/note="compared to the sequence deposited
Accession Number AE003626"
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Pred. No. 9.1e-102;
0; Mismatches 519;
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Accession Number AE003626"
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                                                                     1. .2068
/organism="Drosophila m
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                                                                                                                                      379. .1908
/gene="nAcRalpha-30D"
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/gene="nAcRalpha-30D"
379. .1908
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                                                                                                                                                                                                        /dev_stage="embryo"
1. .2068
                                           Location/Qualifiers
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1605
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Best Local Similarity 62.4%;
Matches 946; Conservative
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Budaryota, Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brackycera; Muscomcrpha;

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 2068)

I (bases 1 to 2068)

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-Mediated A-to-I pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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                                                                                                                                    -----CCGCAAGCGCAGCAGCCGCAATGCTGCCGATAC 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 TACAGGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCACAGTTGCTTCGGTGTCGAC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------TACGAGCTC 1299
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                                                                                                                                                                                                                                            1151 TCTTCTTCGAGTTCCTCCGCCATCCGGCGAGAAGAAGCAACAGATCCAAAACGTTGAGCTC 1210
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                                                                                                                                                                                                     -----ACCTGGAGCTG 1134
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AF321448
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                                                                                                          CCGTGGGTGCTGCGCATGTCACGGCCC------GGCTCGGCGACGCCGCCGCCG
                                                                                                                                                                                                                                                                                          1135 CGCGAGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCTCGACATCGATGACGACTTCCGC
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Grauso, M. and Sattelle, D.B.
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1631 ATTGTG 1636
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Buskaryota: Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilae: Drosophila:
I (bases 1 to 2110)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Micotinic Acetylcholine Receptor Subunit Genes,
Novel Putative Airophila and Dalpha?, in Drosophila melanogaster Identify &
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type V (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
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                                                                                CGACATCGATGACGACTTCCGCCACCCCCAAGCGCAGCAGCCCCCAATGCTGCCGATACTA
                                                                                              1707 CAAAGATCTTCATCTAAATTCTTAAAGAATTGCAATTTATTACGCCGCGGATGCGCAAAGC
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                          TCCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCT
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (
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/chromosome="2"
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SMPPFKTRKSTDTYSTPAATTACPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
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ELDVBLKERSSSKSLLANVLDIDDFRHWCRPWTPGGTLPHNPAPYRTVYGQGDDGSIG
PIGSTRMPDAVTHHOTIKSSTBYELGILIKEIRFITDQLRKDDECNDIANDWKFAAMV
VDRLCLIIFTMFAILATIAVLLSAPHIIVS"
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                                                                                                                                                                                                                                                            Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. Nucleic acids encoding acetylcholin-receptor subunits from insects Patent: EP 0962528-A 1 08-DEC-1999; BAYER AG (DE)
 GGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGG
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Ephydroidea; Drosophilidae; Drosophila
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 1.7e-93;
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/note="unnamed protein product"
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Eukaryota; Metazoa; Arthropoda;
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Search completed: August 21, 2003, 09:54:17 Job time: 5551.39 secs

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APPLICANT: JOHNON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 619-677-1465
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Pred. No. 4.3e-107;
80; Mismatches 117;
                                                           US-09-217-345-4
US-08-487-596-18
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US-08-487-596-4
US-08-471-961-3
US-08-487-596-10
US-08-487-596-10
US-08-487-596-10
US-08-484-722-2
US-08-660-451A-10
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US-08-467-574-12
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US-08-466-589-12
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Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
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Best Local Similarity 46.09
Matches 240; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
; MOLECULE TYPE: protein US-08-278-635B-7
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MEDIUM TYPE: Floppy
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                           GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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SEQUENCE CHARACTERISTICS:
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US-08-464-258B-7
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APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                    ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
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FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08464258B Patent No. 6013766
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-----LASVELSAGAG-
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TELEPHONE: 619-677-1409
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CORRESPONDENCE ADDRESS
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APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN. STEBHEN F.
TITLE OF INVENTION: CLONING SAPERSSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
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                                                                                                                                        29.5%; Score 1191.5; DB 3 llarity 46.0%; Pred. No. 4.3e-107; Conservative 80; Mismatches 117;
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 6100046
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
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NUMBER OF SEQUENCES:
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STREET: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                     354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 KNQVLTINIHLGMSWTDHYLQMNMSEYPGVKNVRFPDGQIWKPDILLYNSADERFDATFH 127
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                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                   DB 3; Length 502;
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TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL

TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                           REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
FORMATION FOR SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SEC
                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOHNSON, DAVID S. BOULTER, JAMES R.
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                     NAME: REITER, STEPHEN E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                         i: 502 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-471-961-7
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                Similarity
                               CLASSIFICATION:
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                                                                                                                                                                                                                                                        TOPOLOGY:
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Matches 240;
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 NGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 511;
                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1168; DB 1;
; Pred. No. 8.5e-105;
83; Mismatches 117;
                 E: GRAY CARY WARE & FREIDENRICH 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                           3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
28.9%;
Best Local Similarity 44.2%;
Matches 238; Conservative 83
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NAME: REITER, STEPHEN E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 amino acids
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                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                   CALIFORNIA
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                                                             SAN DIEGO
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                                                                              665 NPAFYRTVYG------QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
                                                                                                        405 DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                      ------PG----H 387
605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
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                                                                                                                                                             711 LKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/47'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: GRAY CARY WARE & FREIDENRICH 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
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                                        364 SCKY----SYPKHHPSLKNTEM-
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Patent No. 6100046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                   ent No.

JNERAL THOORMATION.

JNEAL SPEICANT: ELGOTHEN, ANA BELLANT: JOHNSON, DAVID S.

TOTAL JOHNSON, DAVID S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: REITER, STEPHEN E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 amino acids
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; MOLECULE TYPE: protein
US-08-471-961-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: CALIFORNIA
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                                                                              APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: HOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 511;
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.9%; Score 1168; DB 3;
44.2%; Pred. No. 8.5e-105;
tive 83; Mismatches 117;
                                                                                                                                                                                                                                              E: GRAY CARY WARE & FREIDENRICH LLP 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTONNEY AGENT INFORMATION:
                   Sequence 8, Application US/08464258B
Patent No. 6013766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 44.2
Matches 238; Conservative
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                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           CALIFORNIA
                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                  ADDRESSEE:
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US-08-464-258B-8
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UMBER: US 08/028,031
08-MAR-1993
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FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ellid, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURON
TITLE OF INVENTION: AUGUSTOR CON
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08700636
Patent No. 5910582
                               Query Match
Best Local Similarity 45.18
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 08-MAR
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US-08-700-636-8
 US-08-466-589-8
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304 YFASIMVIVGLSVVVTVLVLQFHHHDPQAGKMPRWVRVILLLNWCAWFLRMKKPGENIKPL 363
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                                                                                                                                                                                                                                                                                      364 SCKY----SYPKHHPSLKNTEM-----NVL--------H387
                                                                                                                                                                                                                                                                                                                        NPAFYRTVYG------QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
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                                                                                                                    NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNWVAETMPATSDAVPL--- 581
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                  ------RPICWLPWILRMSRPG---RPL
                                                   DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF
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STREET: 1660 Union Street
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIERCATION: 536
PRIOR APPLICATION NUMBER: US 08/028,031
FILING DATE: MATCH 8, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08466589
Patent No. 5837489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STATE: CA
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STRANDEDNESS:
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MOLECULE TYPE:
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12;
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                                                                                                                                      67
                                                                                           297 IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                   474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
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                                                   Gaps
                                               91;
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                                                 Indels
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ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTENT FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    DB 2;
28.7%; Score 1159.5; DB 2; 45.1%; Pred. No. 5.6e-104; tive 82; Mismatches 115;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                 68 KNQVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
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                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
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                                                                                                                                                                                                                                                                                               91;
                                                                                                                                                                                                                                                                DB 2; Length 502,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Brown, Martin, Haller & McClaim
1660 Union Street
          NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-9392
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Patent No. 6022704
                                                                                                                                           LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                           Query Match 28.7%;
Best Local Similarity 45.1%;
Matches 237; Conservative 8
ATTORNEY/AGENT INFORMATION:
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TTY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 GLSVVVTVIVLQYHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.7%; Score 1159.5; DB 3; 45.1%; Pred. No. 5.6e-104; iive 82; Mismatches 115;
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPAX: 610-238-0999
                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
                                                                                  SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
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Matches 237; Conservative
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                        Diskette
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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305 GLSVVVTVIVLQYHHDPDGGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR 363
                                                                                                                                                                                                                                                      245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                               --WIRIVELCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                    613 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                            669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                   364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP--
                                                                                                                                                                                                                                                                                                                      724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL TITLE OF INVENTION: ANTAGONIST SOFT HUMAN NEURONAL TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-NAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08487596 Patent No. 6440681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
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                                                                                  APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 502;
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STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seidman, Stephanie L
REGISTATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-UN-95
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/466,589, FILING DATE: 05-JUN-95 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/028,031 FILING DATE: 08-WAR-93 ATTORNEY/AGENT INFORMATION:
                Sequence 8, Application US/09217345 Patent No. 6303753 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TELEFAX: 619-587-5360
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LENGTH: 502 amino acids
TYPE: amino acid
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Best Local Similarity 45.11
Matches 237; Conservative
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unknown
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                                                                                                                                                                                                                                                                                            La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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us-09-303-232-2.rai

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COMPUTER-READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,C
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seidman, Stephanie
236; Conservative
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92101-2926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
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US-08-496-855A-2
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TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
FILE REFERENCE: 6017.05.01
CURRENT APPLICATION NUMBER: US/08/771,737
NUMBER OF SO ID NOS: 8
SOFTWARE: PSECISO FOR Windows Version 3.0
                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
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                                                                                                                                                                               Gaps
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                                                                                                                     Length 502;
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                                                                                                                                                                            Indels
                                                                                                                  ; Score 1159.5; DB 4;
; Pred. No. 5.6e-104;
82; Mismatches 115;
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Pred. No. 1.4e-103;
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Patent No. 6323000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Briggs, Clark A.
APPLICANT: Gopalakrishnan, Murali
APPLICANT: McKenna, David G.
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APPLICANT: Roch, Jean-Warc
APPLICANT: Sullivan, James P.
APPLICANT: Touma, Edward
APPLICANT: Abbott Laboratories
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45.0%;
                                                                                                                  28.7%;
                                                                                                                                                                         237; Conservative
                           ; MOLECULE TYPE: protein US-08-487-596-12
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   unknown
                                                                                                                  Query Match
Best Local Similarity
Matches 237; Conserv
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Best Local Similarity
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Patent No. 5801232
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                    -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                       474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
  Gaps
91;
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APPLICATION NUMBER: US/08/496,855A
  82; Mismatches 116;
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STREET: 1660 Union Street
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20-JUN-1995
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                                                                                                                                                                                                               DB 1; Length 529;
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APPLICANT: Elliot, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: MTTHOOS FOR HUMAN NEURONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
TUMBER OF SEQUENCES:
TUMBER OF SEQUENCES:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                          21.0%; Score 848.5; DB 1; Length 36.7%; Pred. No. 1.1e-73; ive 87; Mismatches 154; Indels
                  6362-9369B
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Patent No. 6440681
GENERAL INFORMATION:
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33,779
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                            TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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San Diego
                                                                                                              : 529 amino acids
amino acid
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER
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Matches 183; Conservative
                                                                                                                                                         MOLECULE TYPE: protein US-08-496-855A-2
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US-08-487-596-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
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                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.0%; Score 848.5; DB 4; Best Local Similarity 36.7%; Pred. No. 1.1e-73; Matches 183; Conservative 87; Mismatches 154;
                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 08/028,031
08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 529 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-NOV-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 08-MAR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
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409 DAEERE------VVVEEEDRWACAGHVAPSVGTL------CSHGHLHSGASGPKAE 452
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                                                                                                                                                                                                                                                                                                                                                         292 DCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLN 351
                                                                                                                                                                                                                                                 629 ELKERSSKSLLANVLDIDDDFRHNCR-PMTPG-GTLPHNPAFYRTVYGQGDDGSIGPIGS 686
486 ELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLPP
                                                                                                                                                                                                      352 VHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV
                                                                                                                                                                   ---WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILSDV
                                                                               546 DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
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Job time : 25.5314 secs
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                                                                                                                                                                                                                                    APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HOMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.1e-73;
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERNCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                Sequence 2, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANY: Blliott, Kathryn J.
APPLICANY: Harpold, Michael M.
                                        744 LCLIIFTMFAILATIAVLL 762
                                                              : | : | : | : | 503 IFLWLFIIVCFLGTIGLFL 521
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36.7%;
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IBM Compatible
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Matches 183; Conservative
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453 ALLQEGELLLSPH-
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FRAGMENT TYPE: N
ORIGINAL SOURCE:
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US-08-660-451A-2
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COUNTRY:
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Best Local S
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drosophila

062083 Q18556 Q8MUR0 O46133 Q9U941 Q9VC74 O46128 P91765

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August 13, 2003, 15:21:20 ; Search time 73.6446 Seconds (Without alignments) 2698.100 Million cell updates/sec
                                                                             1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770
                                                                                                                         830525
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                            830525 segs, 258052604 residues
                            OM protein - protein search, using sw model
                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                              SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                               US-09-303-232-2
4043
                                                                 Title:
Perfect score:
                                                                                          Scoring table:
                                                                             Sequence:
                                                                                                            Searched:
                                                                                                                                                                                Database
                                         Run on:
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081932 caenorhabdi 081932 caenorhabdi 082083 caenorhabdi 01856 caenorhabdi 08mur0 apis mellif 046133 locusta mig 09u941 myzus persi 09u641 myzus persi 046128 heliothis v 091765 myzus persi 09f631 heliothis v 096631 heliothis v 096632 heliothis v 096632 heliothis v 096632 heliothis v 08109 aplysia cal 081764 myzus persi 041764 myzus persi 041760 mus musculu 08mm21 aphis gossy 091760 mus musculu 08wrs1 chilo suppr 084960 aplysia cal 09633 heliothis v 081544 drosophila 096533 heliothis v 081544 drosophila

096631 096632 Q8T0Y9

046134 P91764 Q9NFX8 O46135

### ALIGNMENTS

Q8MM21 Q91X60 Q8WRS1 Q8T9S0 Q9W3G6

096633 018394 Q8T5F4 Q8VHH6

RESULT 1 Q817V5 ID Q817V5 PRELIMINARY; PRT; 807 AA.		DE Nicotinic acetylcholine receptor Dalpha5 subunit. GN NACR-ALPHA.34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR	 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila.				RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-			DR EMBL; AF2/2//8; AAM1339U.1;   DR FlyBase: FBqn0028875: nAcR-alpha-34E.		н,	DR Interro; IPRU06029; Neu_channel_memb. DR Pfam: PF02931: Neur chan LBD: 1.		DR PROSITE: PS00236: NEUROTR ION CHANNEL: 1.	KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;	NW 11ALISHEHIDLAIDE. SQ SEQUENCE 807 AA; 91223 MW; C8B4F6B34287C8C8 CRC64;	
5: sp_inverters 6: sp_mammal:* 7: sp_mhc:* 8: en_organile:*	9: Sp_phage:* 10: sp_phage:* 11: sp_rodent:*		<pre>1/: sp_archeap:* ed. No. is the number of results predicted by chance to have a</pre>	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	·	Query	4014.5 99.3 807 5 08T7V5 08t7v5 drosophila	59.1 482 5 Q8T5F5	40.2 494 5 (	40.1 494 5 Q8T7S3 .Q8t7s3	5 Q8T7S1 , Q8t7	39.8 501 5	. 509 5 Q8T7S0 Q8t7S0	32.4 554 5 Q9VL79 09v179	1235 30.5 525 5 Q8IPE2 Q8ipe2 drosophila	29.3 5/2 1 29/415 29/4 29.3 5/2 11 09/4106 099 28.9 511 13 003481 003	

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Result

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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID-7227;
                                                                                                                                               EMBL; AY036613; AAK67256.1; -.
Flybase; FBgn0028875; nACR-alpha-34E.
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InterPro; IPR006202; Neur_chan_LBD.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                           482 AA;
                                                  SEQUENCE FROM N.A.
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Q9VWI9;
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                                                                                                                                                                                                                                                         IIILINYHHRNADTHEMSEWIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQ
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                                                           1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSSTRTTSSNQRHNOQLTTLQPRSLSTKH
                              Gaps
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1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit
NACR-ALPHA-34E OR NACRALPHA34E OR BG:DS05899.4 OR BG:DS05899.5 OR
654498 OR CG16879.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Length 807;
                              Indels
           5,
                             ;
           DB
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           Score 4014.5;
Pred. No. 0;
                              Mismatches
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QBT5F5,
01-JUN-2002 (TEMBLEEL 21,
01-JUN-2002 (TEMBLEEL 21,
01-MAR-2003 (TEMBLEEL 23,
          99.3%;
95.4%;
                              Conservative
                    Similarity
                   Local Similar
                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
MEDLINE-21969411; PubMed=11973307; Grauso M., Reenan R.A., Culetto B., Sattelle D.B.; Dubuit Genes, B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphas, and Dalpha7, in Drosophila melanogaster Identify New and Highly Conserved Target of Adenosine Deaminase Acting on Rediated A-to-1 Pre-mRAR Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                             Pfam; PF02931; Neur_chan_LBD; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.1%; Score 2388.5; DB EBest Local Similarity 98.3%; Pred. No. 1.6e-197; Matches 457; Conservative 4; Mismatches 3;
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RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams W.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.E., Gocayne G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Stutton G.G., Worthand J.R., Yandell M.D., Zhang Q., Chen L.X., Radadon R.G., Worthand J.R., Yandell M.D., Zhang Q., Chen L.X., Bardon R.C., Batch R.G., Champe M., Ffeiffer B.D., Radadon R.C., Batch R.G., Champe M., Ffeiffer B.D., Radadon R.C., Boggers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D., Radion R.Y., Doyle C., Batch G.G., Wank K.H., Doyle C., Batch G.G., Wank K.H., Doyle C., Batch B.P., Banderson R.Y., Basun A., Baxendala J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basun A., Batch B.P., Banderson F., Carler B., Bolchan M.R., Boud G.J., Bayraktaroglu L., Belshakov S., Burkis K.C., Busam D.A., Euller H., Cadieu E., Center A., Chandra I., Raderis R.A., Coup E., Dowles M., Dughan-Rocha S., Dunkov B.C., Dunn P. Burtis K.C., Busam D.A., Eulle C., Perraz C., Ferraz C., Ferrar S., Dulkov B.C., Dun P., Harvey D., Heiman T.J., Herris M.L., Harvey D., Heiman T.J., Herris M.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M.L., Harvey D., Heiman T.J., Wei M.-H., Liday Y., Lin X., Lasko P., Lei Y., Levitesky A.A., Li J., Li Z., Liang Y., Lin X., Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hostin D., Houston M.A., Misch M. Murphy B., Murphy L., Muzny D.M., Nelson D.L., Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Spiener K., Wassaman D.A., Wootley K.C., Wu D., Yang S., Yao Q.A., Shiener K., Wassaman D.A., Whorley K.C., Wu D., Yang G., Zhu X., Smith H.O., Walleng R., Zhong R., Shong S., Zhu X., Woodbage T., Wassenbach J., Wang S., Yang R., Shong S., Rhong S., Zhu Y., Warssenbach J., Wars S.
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Banson J., An H., Baldwin D., Banson J., Beeson K.C., Rogers Y.,

Banson J., An H., Baldwin D., Banson J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Refriers S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J. Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacled J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,

William S.M., Strong R., Svirskas R., Tector C., Tyler D.,

William S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
  Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710 ILKEIRFITDQERKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 PDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 SWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII
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                        , Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
butative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003511; AAF48950.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.2%; Score 1988; DB 5; 71.0%; Pred. No. 7.3e-163; tive 46; Mismatches 51;
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                                                                                                                                                                                                                                                                                   InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neur_channel_memb.
Pfam; FF02931; Neur_chan_LBD; 1.
Pfam; FF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
PROSITE; PR00256; NRIONCHANNEL.
PROSITE; PR002165; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 545 AA; 61517 WW; 7B83025107,
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InterPro; IPR006201; Neur_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 QGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schulte T., Oellers N., Adamczewski M.;

Schulte T., Oellers N., Adamczewski M.;

T "Putative alpha subunits of insect nicotinic acetylcholine receptors

T more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than

T to other insect nicotinic acetylcholine receptor alpha subunits.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

C. -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; AF143846; AAD12697.1;

REMBL; AF143846; AAD12697.1;

InterPro; IPR0066202; Neur_channel.

RINTER: PR02931; Neur_chan_LBD.

R Pfam; PF02931; Neur_chan_LBD.

R Pfam; PF02932; Neur_chan_LBD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPRRVPPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                     LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                      DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---WIRIVFLCWLPWILRMSRPG---RPLILEFPTTPGS
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL-------
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                            Length 496;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                     496 AA; 56347 MW; 8032FED8515A6210 CRC64;
                                                                                                                                                                                                                                                             Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS 770
                                                                                                                                                                                                                                                                                                          45.8%; Score 1850; DB 5; 70.0%; Pred. No. 5.3e-151; 1ve 30; Mismatches 49;
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                                                                                                                                                                                                                                                  PROSITE; PS00236; NEUROTR_ION_CHANNEL;
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                                                                                                                                                                                                                                       TIGR00860; LIC; 1
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                         SEQUENCE FROM N.A.
                                   NCBI_TaxID=7102
                                                                                                                                                                                                                                                                        ransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8T7S2;
01-JUN-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                 361;
                                                                                                                                                                                                                                       TIGRFAMS;
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                                                                                                                                                                                                                                                                                                            Query Match
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Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8T7S2
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Created)
Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SGSOTAIGSSASFGRPTTVEEHHTAI-GCNHKDLHLILKELQFITARMRKADDEA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SLFVLLIFLAIIKESC-OCPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPC
                                                                                                                                                                                                                        SDTSSERKHQILS --- DVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY
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                       II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                  Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 FMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKI-
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant ty
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygg
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.2%; Score 1625.5; DB 5; 61.4%; Pred. No. 1.3e-131; ive 47; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                         MEDLINE=21969411; PubMed=11973307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56048 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.2%
Best Local Similarity 61.4%
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 AA;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SGSQTAIGSSASFGRPTTVEEHHTAI-GCNHKDLHLILKELQFITARMRKADDEA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKEIRFITDQLRKDDECN 728
                                                                                                                                                                                                                                                                                                                                           ς
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21969411; PubMed-11973307; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Geliting."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 FWVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLQWLPWILRWGRPGRKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDTSSERKHQILS----DVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321445; AAM13392.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                             type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro: IPR006029; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
IIGRPAMS; TIGR00860; LIC; 1.
FNOSITE; PS00236; NEUROTR_LON_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant ty
NACR-ALPHA-30D OR NACRALPHA-30D OR ECDNA:GH0110 OR CG4128.
                                                                                                                                                                                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.1%; Score 1622.5; DB 5; Length 61.2%; Pred. No. 2.3e-131;
ive 46; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 AA; 56095 MW; B46EBEDA63A92942 CRC64;
                                                                 494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0032151; nAcR-alpha-30D.
                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 61.23
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 494;
                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
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56113 MW; 48327537229573FF CRC64;
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61.0%; Pred. No. 3.5e-131
tive 49; Mismatches 75
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                                                                                         494
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InterPro; IPR006202; weur_channel_memb.
Pfam; PF02931; Neur_chan.LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREPMS; TIGRO0860; LIC; 1.
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FlyBase; FBgn0032151; nAcR-alpha-30D.
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Matches 318; Conservative
                                                                                         PRELIMINARY;
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Q8T7S1;
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Oy	BY 614 SDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY 669	Db 249 VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAESM
qa .	360	Оу 582
Qy	670 RTVYGQGDDGSIGPIGSTRMPDAV-THHT	Db 309 TVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVV
qa	399SGSQT	Qy 585 IVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILS
QY		Db 369 SVFLQWLDWILRWGRPGRRITRKTILLS
q	0b 453 ELICDWKFAAMVUDRFCLIVFTLFTIIATVTVLLSAFHIIV 493	Qy 641 NVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIG
RE	RESULT 8	413 NVLDLDDDFRALLT
SA	001/R9  ID 0917R9  PRELIMINARY; PRT; 523 AA.	
£ 5 }		* C
DI DE	<pre>NY 01-JUN-2002 (TrEMBLE-1. 21, Last sequence update) NT 01-MAR-2003 (TrEMBLE-1. 23, Last annotation update) B Nicotinic acetylcholine receptor Dalpha6 subunit variant type V.</pre>	OY (10 VLSAPALIV 709 
ចីទី	NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128. Drosophila melanogaster (Fruit flv).	
888	OC 'Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila,	RESULT 9 Q9XZI4 ID Q9XZI4 PRELIMINARY; PRT; 501 AA.
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Z Z		
R. R.		
R.	RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dit
R. R.		
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<u>a</u> <u>a</u>	DR EMBL; AF321449; AAM13396.1; DR FlyBase; FBgn0032151; nAcR-alpha-30D.	
ā <b>ä</b>		
<u>a</u> 6		
66		CC -:- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CDR EMPH.: AF143847: AAD32698.1: -
ត់គឺនឹ		
2 <b>5</b> 2 0	KW Transmembrane. CO SEDIENCE 53 AB 59110 MW. 1000AF74F87F841 CRC64.	DR InterPro; IPN000629; Neu_channel_memb. DR Pfam: PF02911: Neur chan LBD: 1.
Ď.	SEKOENCE SES ON.	
	Similarity 58.2%; Pred. No. 2.5e-130; Conservative 46; Mismatches 76; Indels	TIGREAMS; TIGROOB60; LIC; 1. PROSITE; PS00236; NEUROTR_ION
δλ		tein; Ionic channel; Po brane.
ŭ	DD 10 SLFVLLIFLAIIKESC-QGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID 68	SEQUENCE 501 AA; 56/04 MW
ි	QY 351 VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIMKPDVLMYNSADEGFDG 410	atch cal Similarity 60.8%;
ប	DD 69 VDEKNQILTTNAWLNEWNDYNERWNETEYGGVKDLRITPNKLWRPDVLMYNSADEGFDG 128	Matches 319
ð	Qy 411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470	QY 299 LLIILINDANACLAGIREARADDILLIINILERIY VANESOT 
ប	DD 129 TYHTNIVVKHNGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNS 188	יט ר
á	471 ETGGDISSYVENGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPC	99
፩	Db 189 EDGGDLSDFITNGEWYLLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVPC 248	Qy 415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGS
ŏ	Qy 531 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581	Db 126 NVVVRSGSCLXVPPGIFKSTCKMDIAWFPFDDQHCDMKFG

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Indels 84; Gaps 10;
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|LNYHHRTADIHEMPPWIK 368
                                         SPIGSTRMPDAV-THHTCI 699
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alpha subunits.";
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IN (BY SIMILARITY).
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trysia; Noctuoidea;
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                                                                                                                                                      SWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII
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                                                                 PDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomontan M.A., Mazda P., Noshrefi A.R., Moshrefi M.,
Nixon K., Paoleb J.M., Park S., Pfeiffer B., Poon L., Squeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AEG03408; AAF44854.1, ...
FIYBase; FB900028875; nAcR-alpha-34E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K. Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 44.0 kDa protein.
NACR-ALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Dittera; Brachycera; Endopterygota; Dittera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
MEDLINE-99403001; PubMed=10471707;
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                                                                                                                                                                                                                                                                                   672
                                        306 SSVVLTVVVLNYHHRTADIHEMPQMIKSVFLQMLPMILRMSRPGKKITRK---TIMMNTR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21969411; PubMed-11973307;

MEDLINE-21969411; PubMed-11973307;

A Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

The analysis of the control of the component of th
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                                                                                                                                                                                                                                                                                                                                                                                                291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID 350
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                    DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                          ------WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                                                                                                                                                                            618 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                                                                                                                                                                                                                       673 YGQG------DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 23, Last annotation update)
01-MAC-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
BUNATYOCA: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
CALLTAXID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
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Pred. No. 1.4e-129;
8; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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59.38;
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318; Conserv
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REALINE-20196006; PubMed=10731132;

REDLINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.E.,

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RA Amanatides P.G., Barter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Clampe M., Pfeliffer B.D.,

RA Aril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA Doslor K.J., Evangelista C.C., Ferraza C., Ferriers S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Liankulow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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                                                                             1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                 HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                     Gaps
                                                     5;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
064128 protein.
MACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                         Length 391;
                                                     Indels
 E2AB465CF275E8C0 CRC64;
                       94.4%; Pred. No. 4.2e-121; ive 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                    301 NLSAKGECHLNYLECCMQH 319
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43974 MW;
                                      Best_Local Similarity 94.4
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
391 AA;
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SEQUENCE
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Barns C.A., Gocayne J.D., Amenatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR006029; Neu_channel_memb
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Best Local Similarity 47.9%
Matches 286, Conservative
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RAY MEDLINE-20196006; PubMed-10731132;

RAdams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., LiP.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., LiP.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., LiP.W., Hoskins R.A., Galle R.F.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Braindon R.C., Baxter E.G., Champe M., Hoskor C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Barwandale J., Bayraktaroglu L., Beasley E.M.,

RA Barlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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Bonzbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Alaris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck, J.,

Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mepherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                       653
597
                                                                                                                                                                                                                                                                                                                                           353 VSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLQWLPWILRM 412
                                                                                                                                                                                                                                                                                                                                                                                                        654 RPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILK 712
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---ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKPCRRVHA
                                                                                                                                                                                                                                                  293 DNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAERVTILLSLTVFLNLVAETLPQ
                                                                                  | ||||| : |||| ||| || EDGGDLSDFITUREMYLLGYHAGKEEYDSLRLLPRITCRYHLYYT-NSSPYI-----
                                                                                                                                                                                                                                                                                                         --WIRIVFLCWLPWILRM
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                                                                                                                                         RRRTLYYFFNLIIPCVLIASM-----ALLGFTLPPDSGE--------
                                                                                                                                                                                                                           -----KLSLG------VTILLSLTVFLNMVAETMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
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Last sequence update)
Last annotation update)
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                                                             ETGGDISSYVLNGEWELLGV-PGK-----
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
CG4128-PC.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K.S., San S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syirskas R., Tector C., Turner E., Wang A.H., Wang X.,
Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X.,
Milliams S.M., Moodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
A Ha.R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
A cheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Riche R.P., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy M., Park S., Patel S., Pfeiffer B.,
A Pacleb J., Paragas Pittman G.S., Patel S., Pfeiffer B.,
A Stapleton M., Strong R., Syirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003626; AAN10709.1; -. SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Gamer M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Gacrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
RA Ballew R.M., Basu D.A., Burler B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler E., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkoy B.C., Dunn P.,
RA Dodson K., Cabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Ratazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rhenert K., Schen F., Saunders R.D.C., Scheeler F., Shen H.,
Rhenert K., Shen B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                        292
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                                                                                                                      293 DNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAESTYFNCIMFMVASSVVLTVVV 352
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                                                                                 --- LGVTI -------LLSLTVFLNMVA
                                                                                                                                                                   ---ETMPATSDAVPLWIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILS
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NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
CG4498 OR CG16878.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
RRRTLYYFFNLIIPCVLIASM -----ALLGFTLPPDSGEKLS-
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=20196006; Pubmed=10731132;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
Carlson J.W., Center B. Mannee M., Davenport L.B., Dietz S.M.,
Carlson J.W., Center B., Calle R.F., Carg N.S., George R.A.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
R. Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
R. Apoleb J., Paragas V., Park S., Patel S., Pfelifer B.,
Pacleb J., Paragas V., Park S., Patel S., Pfelifer B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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"Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR066202; Neur_chailbD.
InterPro; IPR006029; Neur_chailbD.
Ffam; PF02931; Neur_chailbD; 1.
Pfam; PF02932; Neur_chailbD; 1.
PRINTS; PR00252; NRIONCHANNEL.
PROSTIE; PS00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 273 AA; 31655 MW; CA95F19953B37248 CRC64;
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HSSP; P58154; 119B.
Flybase; FBgn0028875; nAcR-alpha-34E.
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57.2%;
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Submitted (SEP-2002)
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LIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLWIRI 585
                                                                                                                                                                                               |------SEWLRKDDECNDIANDWKFAAMVVDRLCLIFFTMFTILATIAVLLSAP 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stitzel J.A.;

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

C. 1- SUBCELDULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. 1- SUBCELDULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

DR MGD: MGI-99779; Chrna7.

DR MGD: MGI-99779; Chrna7.

DR InterPro; IPR006201; Neur_channel.

DR InterPro; IPR006202; Neur_channel_memb.

DR InterPro; IPR006202; Neur_channel_memb.

DR PRIM: PF02931; Neur_channel_memb.

DR PRIM: PF02931; Neur_channel.il.

DR PRIM: PF02931; Neur_channel.il.

DR PRIM: PF02931; Neur_channel.il.

DR PRIM: PF02932; Neur_channel.il.

DR PRIM: PF02932; Neur_channel.il.
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                                                          586 VFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDI
                                                                                                                    646 DDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEY
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              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stitzel J.A., Farnham D.A., Collins A.C.;
"Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain.";
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PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.3%; Score 1185.5; DB 11; Lengt
46.6%; Pred. No. 1.3e-93;
ive 79; Mismatches 115; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor subunit alpha 7.
                                                                                                                                                                                                                                                                                                                                                 502 AA
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                                                                                    ----LILNY----
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MEDLINE=97189245; PubMed=9037516;
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nes 243; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 CSDTSSERKHQILSDVELKERSS-KSLLANVLDIDDDFR----HNCRPMTPGGTLPHNPA 667
TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                      474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        727 CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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Search completed: August 13, 2003, 15:29:07 Job time : 76.6446 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 13, 2003, 15:14:55; Search time 16.1234 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV.....MFAILATIAVLLSAPHIIVS 770

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		ption	mus musculu	qall	rattus	homo sa	bos t	_	_			homo sapien	homo	droso	drosop	gallus	gallus	gallus	rattus	rattus		carassius a	-				homo sapien	mus musculu	xenopus lae	rattus norv	caenorhabdi	rattus norv			
•		Description	58	P22770	005941	P36544	P54131	P48180	P09478	P91766	P23414	Q15822	P32297	P17644	P04755	P09480	P09479	P09481	P12389	P04757	007263	P18845	P25162	P30926	P49581	P02709	015825	P04756	P05377	P43143	P45963	P25108	P26153	94	098880
SUMMARIES		TD	ACH7_MOUSE	ACH7_CHICK	ACH7_RAT	ACH7_HUMAN	ACH7_BOVIN	ACH1_CAEEL	ACH1_DROME	ACH1_MANSE	ACH1_SCHGR	ACH2_HUMAN	ACH3_HUMAN	ACH2_DROME	ACH3_DROME	ACH2_CHICK	ACHA_CHICK	ACH3_CHICK	ACH2_RAT	ACH3_RAT	ACH3_BOVIN	ACH3_CARAU	ACH4_DROME	ACHP_HUMAN	ACH6_CHICK	ACHA_BOVIN	ACH6_HUMAN	ACHA_MOUSE	ACH2_XENLA	ACH6_RAT	ACH8_CAEEL	ACHA_RAT	ACHP_CHICK	ACHN_CHICK	ACHA_BRARE
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		Score	1182.5	1179.5	1173.5	1159.5	1157	1104	888	986	873	848.5	845	843.5	840	838	827.5	827.5	827	823	820.5	820.5	815.5	802	803	801	799	797	794.5	792.5	791.5	789	789	7	786.5
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P02	P12	P12	P17	P02	P43	P09	P02	P22	P12	P19	60d
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461	495	500	502	482	627	622	461	457	464	459	630
19.4	19.4	19.4	19.3	19.3	19.3	19.3	19.3	19.1	19.1	19.0	19.0
785	783	782.5	782	780	780	779.5	779	773.5	772	769.5	768
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ACH7, WOUSE STANDARD; P49582; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 31, Last seq 28-FEB-2003 (Rel. 41, Last ann Neuronal acetylcholine receptor CHRNA7 OR ACRA7. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. STRAIN-BALB/C; TISSUE-Brain; MEDLIRE-95324936; Pubmed=76014 Orr-Urreger A., Seldin M.F., "Cloning and mapping of the mo acetylcholine receptor"; Genomics 26:399-407(1995)		ACH7_MOUSE							
•	QI.	ACH7_MOUSE	STANDA	.RD;	PRT;	205	AA.		
	A E	P49582;		4					
	55	01-FEB-1996		Last se	, quence u	pdate	á		
	Ы	28-FEB-2003	(Rel. 41,	Last an	notation	pdn	ate)		
	DE	Neuronal ace	tylcholin	e recept	or prote	in,	alpha-7 c	hain prec	ursor.
	GN	CHRNA7 OR AC	RA7.						
	SO	Mus musculus	(Mouse).						
	ဗ	Eukaryota; M	etazoa; C	hordata;		a; V	ertebrata	; Euteleo	stomi;
•	ဗ	Mammalia; Eu	theria; R	odentia;		inath.	i; Murida	e; Murina	e; Mus.
	ŏ	NCBI_TaxID=1	0600;						
	Z.	[1]							
	RP.	SEQUENCE FRO	M N.A.						
	<u>ي</u>	STRAIN-BALB/	c; TISSUE	-Brain;					
	ž	MEDLINE=9532	4936; Pub	Med=7601	470;				
	RA E	Orr-Urtreger	A., Seld	in M.F.,	Baldini	Ā	Beaudet	A.L.;	
	F 5	"Cloning and	mapping	ot the m	onse alf	ha 7	-neuronal	nicotini	Ö.
•	Z :	acetylcholin	e recepto	r. ";					
	Z.6	Genomics 26:	399-402(I	995).					
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	ပ္ပ	EXTENSIV	E CHANGE	IN CONFO	RMATION	THAT	AFFECTS	ALL SUBUN	ITS AND
	ع د	MEMBEANT	OFFINIO	OF AN 10	N-CONDOC	PILI	CHANNEL	ACKUSS TH	E PLASMA
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	20	SIMILARI	TY).		: }			2	
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	ည		TY: BELON	GS TO TH	E LIGANE	-GAT	ED IONIC	CHANNEL F.	AMILY.
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	္ပ	This SWISS-P	ROT entry	is copy	right. I	tis	produced	through	a collaborati
The European Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb.sib.ch/annouror send an email to license@isb-sib.ch).  EMBL; L37663; AAC42053.1;	၂ (	between the	Swiss In	stitute	or Bioin	torm	atics an	d the EM	BL outstation
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modifies requires a license agreement is not removed. Usage by entities requires a license agreement (See http://www.is or send an email to license@isb-sib.ch).  EMBL; L37663 AAC42053.1;	ပ္ပ	use by non	-profit	institut	ions as	long	as its	content	
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EMBL; L37663; AAC42053.1; PIR; A57175; A57175. MGD; MGI:99779; Chrna7. InterPro; IPR006029; Neur_chan InterPro; IPR006202; Neur_chan InterPro; IPR006201; Neur_chan Pfam; PF02931; Neur_chan_LBD; Pfam; PF02932; Neur_chan_memb PR0375; PR00252; NRIONCHANNEL TIGRFAMS; TIGR00860; LIC; I. PROSITE; PS00256; NEURCHANNEL Transmembrane; Ionic SIGNAL 23 502	ع ر	יייייייייייייייייייייייייייייייייייייי		דרכוומכיד	orte de		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	
PIR: A57175; AFA-22-03-1; PIR: A57175; AFA-22-03-1; MGD; MGI: 99779; Chrna7. InterPro; IPR0066202; Neur_chan InterPro; IPR006202; Neur_chan Pfan: PF02931; Neur_chan_memb PRINTS; PR00252; Neur_chan_memb PRINTS; PR00252; NRIONCHANNEL TIGRRAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NERGYR ION POSTSYNAPTIC membrane; IONIC Transmembrane; Multigene fami SIGNAL 23 502	3 2	PMDI. 137662	3004244						
MGD; MGI:99779; Chrna7. InterPro; IPR006029; Neu_chan InterPro; IPR006201; Neu_chan InterPro; IPR006201; Neu_chan InterPro; IPR006201; Neu_chan Pfam; PF02931; Neu_chan_EBD; Pfam; PF02932; Neu_chan_memb PRINTS; PR00252; NRIONCHANNEL TIGRFAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NEUROTR_ION POSTSYNAPTIC membrane; IOnic Transmembrane; Multigene fami SIGNAL CHAIN 23 502	<u> </u>	DIR: A57175:	A57175	1					
InterPro; IPR006029; Neu_chan InterPro; IPR006029; Neur_cha InterPro; IPR006201; Neur_cha Pfam; PF02931; Neur_chan_LBD; Pfam; PF02932; Neur_chan_LBD; PRINYS; PR00252; NRIONCHANNEL TIGRFAMS; TIGR00860; LIC; 1. PROSITE; PS00256; NEUROTR_LON POStSynaptic membrane; Ionic Transmembrane; Multigene fami SIGNAL 23 502	2 2	MGD: MGT: 997	79: Chrna	7					
InterPro; IPR006202; Neur_chan InterPro; IPR006201; Neur_chan InterPro; IPR006201; Neur_chan Pfam; PF02931; Neur_chan_memb PRINTS; PR00252; NRIONCHANNEL TIGRPAMS; TIGR00860; LIC; I. PROSITE; PS00236; NEURCYR_ION POSTSYNAPTIC membrane; IONIC SIGNAL 1 22 CHAIN 23 502	. A	Interpro: ID	R006029 ·	New Chan	dmem ler			·	
InterPro; IPR006201; Neur_chan Pfam; PF02931; Neur_chan_LBD; Pfam; PF02932; Neur_chan_memb PRINTS; PR00252; NRIONCHANNEL TIGRRAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NEUROTR_ION POSESynaptic membrane; Multigene fami SIGNAL 1 22 CHAIN 23 502	2 2	InterPro: IP	R006202	Neur cha	תביז ר				
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Pfam; PF02932; Neur_chan_memb PRINYS; PR00252; NRIONCHANNEL TIGRFAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NEURONTR_ION POStSynaptic membrane; Ionic Transmembrane; Multigene fami SIGNAL 1 22 CHAIN 23 502	ä	Pfam: PF0293	1: Neur c	han LBD:	1				
PRINTS; PR00252; NRĪONCHĀNNEL TIGRRAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NERGOTR ION POSTSYNAPTIC MEMbrane; IONIC SIGNAL 1 22 CHAIN 23 502	Z Z	Pfam; PF0293;	2; Neur c	han memb	; ;				
TIGRFAMS; TIGRO0860; LIC; 1. PROSITE; PS00236; NEUROTR_ION POSTSYNAPLIC membrane; Ionic Transmembrane; Multigene fami SIGNAL 1 22 CHAIN 23 502	DR	PRINTS; PROO	252; NRIO	NCHANNEL					
PROSITE; PS00236; NEUROTR_ION POSESYNAPTIC membrane; IOnic Transmembrane; Multigene fami SIGNAL 1 22 CHAIN 23 502	DR	TIGRFAMS; TIC	3R00860; 1	LIC; 1.					
Postsynaptic membrane; Ionic Transmembrane; Multigene fami SIGNAL 1 22 CHAIN 23 502	DR	PROSITE; PSO	0236; NEU	ROTR_ION	CHANNEL	٠; ۲			
Transmembrane; Multigene fami SCIGNAL 1 22 CHAIN 23 502	Σ×	Postsynaptic	membrane	; Ionic	channel;	Glyc	coprotein		
SIGNAL 1 22 CHAIN 23 502	<u>×</u>	Transmembran	e; Multig	ene fami.	ly.				
CHAIN 23 502	E E	SIGNAL	٠		BY SIMIL	ARITY	,		
DOMATM 22		CHAIN			NEURONAL MEDHA-7	ACET	PYLCHOLIN	E RECEPTOR	R PROTEIN,
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                   Gaps
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MEDLINE-91097796; Pubmed-1702646;
Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
Millar N., Valera S., Barkas T., Ballivet M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                  POTENTIAL.

BY SIMILARITY.

ASSOCIATED WITH RECEPTOR ACTIVATION

(BY SIMILARITY).
                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
C9312E5226D120E3 CRC64;
                                                                                                                                                                                                   85;
                                                                                                                                                                         DB 1; Length 502;
                                                                                                                                                                                                 80; Mismatches 118; Indels
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                                                                                                                                                                                      Pred. No. 2.8e-75;
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                                                                                                                                                                       29.2%; Score 1182.5;
                            POTENTIAL
                                                                                                                                             56631 MW;
                                                                                                                                                                                     45.8%;
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 255
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133
                                                                                                                                             502 AA;
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 231
262
296
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470
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133
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P22770;
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neuronal nicotinic acetylcholine receptor subunit (alpha 7) is relopmentally regulated and forms a homo-oligomeric channel blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Brain;
MEDLINE-85270494; PubMed=3860855;
Conti-Troncon1 B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., La1 F.A.,
                                                                                                                                                                                                                                                                                                                                                                                   "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-92049732; PubMed=1719423; Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; "Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.

MEDLINE=93024917; PubMed=1383829;
Galzī J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
Changeux J.-P., Bertrand D.;
Mutations in the channel domain of a neuronal nicotinic receptor
convert ion selectivity from cationic to anionic.";
Nature 359:500-505(1992).

-I- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LIADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPMENTY STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                              Lindstroem J.;
and MAbs reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                             Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
                                                                                                                                                         Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J. "Brain alpha-bungarotoxin binding protein cDNAs and MAbs reve subtypes of this branch of the ligand-gated ion channel gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologous proteins.";
Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
                                                                                                                                                                                                                                                                                                       STRAIN-White leghorn; TISSUE=Erythrocyte;
MEDLINE=93049204; PubMed=1425587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                  developmentally regulated and forms
                                                                                                                                      MEDLINE=90315158; PubMed=2369519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 11:4529-4538(1992).
                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-18 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinic receptor.";
Nature 353:846-849(1991).
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                                                        5:847-856(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JN0113; JN0113.
1KC4; 17-APR-02.
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                                                                                              SEQUENCE FROM N.A.
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                                                                                                                   TISSUE=Brain;
                                          by alpha-BTX.
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                                                           Neuron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCS
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                                                                                                                                                                                                                                                                                             NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;. Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . ) (POTENTIAL).
L-S,T: SUPPRESSES INHIBITION BY THE OPEN-CHANNEL BLOCKER QX-222.
QR -> ET (TN DEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                 InterPro: IPRO00029; Neu_channel_memb.
InterPro: IPR006202; Neur_chan_LBD.
InterPro: PR006201; Neur_chan_LBD.
InterPro: PR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_memb.
PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 10.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS00236; Neurorr_ION_C channel; Glycoprotein; Signal; Transmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 4.6e-75;
80; Mismatches 127; Indels
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572325D4309AD2FD CRC64;
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502 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION. AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBMINITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-93147931; PubMed-7678857;
MEDLINE-93147931; PubMed-7678857;
Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
Sequelar Choning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
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ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
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PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL)
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PIR; T01378; T01378.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUE=Brain;
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Interpro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
PRT;
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                                                                                              CHRNA7 OR ACRA7.
Rattus norvegicus (Rat).
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502
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FROM N.A.

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MEDLINE=97062879; PubMed=8906617; Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; Chavez Noriega L.E., Imman neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
        TISSUE-Hippocampus;
Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                        beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                         SEQUENCE FROM N.A.
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                                                                                                                                                     SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
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TNVLVNASGHCQYLPPGIFKSCYIDVRWFPFDVQQCKLKFGSWSYGGWSLDLQMQE---
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       (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P36544; 015826; 096RH2; 099555; 09BKH0; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuronal acetylcholine receptor protein, alpha-7 chain precursor. CHRNA7 OR NACHRA7.
                                                                                                                  85;
                                                                                           Score 1173.5; DB 1; Length
Pred. No. 1.2e-74;
                                                                                                                   119; Indels
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21818878; PubMed=11829490;
REILEY B., Williamson M., Collier D., Wilkie H., Makoff A.;
"A 3-Mb map of a large segmental duplication overlapping the alpha7-
nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
Genomics 79:197-209(2002).
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SEQUENCE FROM N.A.

MEDILINE-97162233; Pubmed=9009220;

Groot Kornelink P.J., Luyten W.H.M.L.;

Groot Kornelink P.J., Luyten W.H.M.L.;

"Cloning and sequence of full-length cDNAs encoding the human neuro nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 a expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";

FEBS Lett, 400:309-314(1997).
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Proteomics 2:212-223(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
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MEDLINE=21829512; PubMed=11840567;
Marris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
Zvelebil M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cluster analysis of an extensive human breast cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti
Heinemann S.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arredondo J., Grando S.A.; "Cloning cholinergic receptors in human keratinocytes."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                         Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nicotinic receptor subunit gene (CHRNA7)."; Genomics 19:379-381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94245214; PubMed=8188270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drug Dev. Res. 30:252-256(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Epidermal keratinocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-502 FROM N.A.
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Name=Short;
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P54131;
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; GO:0000187; P:activation of MAPK; TAS. GO:0006832; P:small molecule transport; TAS.
             SUBCELLUIAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: MW-54157.68; METHOD-MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
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N-LINKED (GLCNAC. . ) (POTENTIAL).
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Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1e-73;
82; Mismatches 115; Indels
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D94B3A482EAA0E42 CRC64;
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A -> G (IN REF. 1 AND 7).
S -> N (IN REF. 2 AND 6).
S -> P (IN REF. 2 AND 6).
C -> S (IN REF. 8).
A -> G (IN REF. 1).
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
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                                                                                                                                                                                                                                                                                                                            L25827; -; NOT_ANNOTATED_CDS. 223141; CAA80672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02923; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
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SIGNAL 1 22 BY S
CHAIN 23 502 NEUF
                                                                                                                                                                                                                                                                                      EMBL; Y08420; CAA69697.1; -- EMBL; AF885858; ARK68111.1; -- EMBL; L2527; -; NOT_ANNOTATED EMBL; Z23141; CAA80672.1; -- EMBL; AF832758; AAK19515.1; -- PIR; G02299; G02259
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                          669 YRTVYGOGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                         GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                  534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                           --WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gutierrez L., Criado M.;
"Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
chromaffin cells: molecular cloning, functional expression and
alternative splicing of the alpha 7 subunit.";
Eur. J. Neurosci. 7:647-655(1995).
-!- FUNCTION. AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN COMPOWATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
TISSUB-Addreal medulla,
MEDILINE-95346009; Pubmed-7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYHHHDPDGGKMPKWTRVVLLNWCAWFLRMKRPG-----EDKVRPACQHNERRCS--LAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628 VELKE-RSSKSLLANVLDIDDDFR----HNCRPMTPGGTLPHNPAFYRTVYGQGDDGSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                          InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_channel_memb.
InterPro; IPR006202; Neur_channel.
InterPro; IPR006202; Neur_channel.
Pfan; PF02931; Neur_chan_LBD; 1.
Pfan; PF02932; Neur_chan_LBD; 1.
Pfan; PF02932; Neur_chan_mb; 1.
PRINTS; PR00223; NEURORHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEURORF, ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%; Score 1157; DB 1; Length 49:46.4%; Pred. No. 1.7e-73;
tive 76; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in isoform Short).
P_000075.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEE5D0B3820D42D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
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                                                                                                                    EMBL; X93604; CAA63802.1; -..
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Best Local Similarity 46.4%
Matches 235; Conservative
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161
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DISULFID
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                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                             Ballivet M., Alliod C., Bertrand S., Bertrand D.; "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR EACHTON: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R PRIX; 568289; 568589.
R PRIX; 568589; 568589.
R HSSP, P58154; 1198.
R WOYNDED; F2566.3; CE09639.
R InterPro; IPR006202; Neu_channel_memb.
R InterPro; IPR006202; Neur_chan_LBD.
R InterPro; IPR006202; Neur_chan_LBD.
R Pfam; PF02931; Neur_chan_LBD; 1.
R Pfam; PF02932; Neur_chan_memb; 1.
R PKINTS; PR00252; NRUNCHANNEL; 1.
R PKINTS; PS00252; NRUNCHANNEL; 1.
R PROSITE; PS00256; NEUROTR_LON_CHANNEL; 1.
R RECEPLOT; POSLSYBAPLIC membrane; Ionic channel; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTEWTIAL).

N-LINKED (GLCNAC. .) (POTEWTIAL).
                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                      498 AA
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 DRLCLIIFTMFAILATIAVLLSAPHII 768
                 ||||||: |::| || || :|||: || 465 DRLCLMAFSVFTILCTIGILMSAPNFV 491
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                                                                                                       PRT;
                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
MEDLINE-96196478; PubMed-8627624;
                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol. 258:261-269(1996)
                                                                                                                                 -FEB-1996 (Rel. 33, Created)
-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X83887; CAA58764.1;
                                                                                                       STANDARD;
                                                                                                                                                                                                          Caenorhabditis elegans.
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498
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252
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93
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E463ABB40AC9FA82 CRC64;

57169 MW;

498 AA;

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                                                                                                                    NOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT 414
                                                                                                                                                                               NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474
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                                                                           -----TIRINETCHTHEFPTTPCSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006, PubMed=10731132;
MEDLINE=20196006, PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bossy B., Ballivet M., Spierer P.; "Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems.";
                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909478; 09VC74; 10, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Ditera; Brachycera; Endopterygota; Ditera; Erachycera; Muscomorpha; Ephydroidea; Drosophila.
                                                                                                                                                                                                                                                                                                    534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
 Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 1104; DB 1; Length 4 43.3%; Pred. No. 8.6e-70; Live 76; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Oregon-R;
MEDLINE=88283626; PubMed=2840281;
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. 7:611-618(1988).
              Best Local Similarity
Matches 227; Conserv
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Query Match
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A. An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahke C., Perrara C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Alorin N.J., Harvey D., Heiman T.J., Hernandez J.F., Houston K.A.,
Alarvis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.B.,
RA Jakop P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Milshina N.V., Mobarty C., Morles O. M., Pill M. N.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Morles D. J.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shier B.C., Staplector K., Tunner R., Wang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worles K.C., Man G., Zhao G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: CNS IN EMBRYOS.
-:- DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR LARVAE STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOODOME BIOL. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Baith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.I Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement ((or send an email to license@isb-sib.ch)
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Flybasę; Fbgn0000036; nAcR-alpha-96Aa.
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
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MEDLINE-22426069; PubMed-12537572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ALPASHRFDLAAAGGISAHCFAEPPLPSSLPLPGADDDLFSPSGLNGDISPGCCPAAAAA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 YTVNLIIPCVGISFLSVLVFYLPSDSGEKISLCISILLSLTVFFLLLAEIIPPTSLTVVPL
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00522; NEUCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS04391; NEUROTR_ION_CHANNEL; 1.
Transmembrane; Multigene family; Polymorphism.
Signal; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                             ------EEPEEDQPPEVLTDVYHLPP------DVDKFVNYDSKRFSGDYGIP
                                                                                                                                                                                                                                                                                                                                                                                                           291 SWIFLLIYLNLS-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQII
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                                                                                                                           ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      ; Score 888; DB 1; Length 567;
; Pred. No. 1.3e-54;
91; Mismatches 168; Indels 102;
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08E1F721FB2A92AC CRC64;
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N-LINKED (GLCNA
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EXTRACELLULAR
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521 IACVVGTALIILQAPSL 537
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35.2%;
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538
108
567 AA;
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DISULFID
DISULFID
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VARIANT
CONFLICT
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516 AA.

PRT;

STANDARD;

ACH1\_MANSE ID ACH1\_MANSE

RESULT 8

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                      Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGRO0860; LIC; 1.
PROSTIE; PS00236; NEUROTR,ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUT. J. NOUNCOSCI. 10:879-889(1998).

EUT. J. NOUNCOSCI. 10:879-889(1998).

EUT. J. NOUNCOSCI. 10:879-889(1998).

EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
P91766;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARAI).
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LIKE CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEMBRANE (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P., Reynolds S.E., Wolstenholme A.J., Wonnacott S., "Characterization of a nicotinic acetylcholine receptor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED WITH RECEPTOR ACTIVATION
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E7A71E8C45D13BD2 CRC64;
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36.6%; Pred. No. 1.5e-54;
ive 65; Mismatches 141; Indels 138;
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98424077; PubMed=9753155;
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Transmembrane; Multigene family
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516 AA;
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                                                                     526
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              NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                           -----WIRIVFLCWLPWILRMSRPGRPLILEFP
                                                                                                                                                                                                                                   TTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY
                                                                                                                                                                                                                                                                                                        TEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLL
                                                                                                                                                                                                                                                                                                                                                              -- PELHKAIDGINYIADQTRKEEESTRVKEDHKYVAMYLDRPFLWIFTLAVVVGSAGIIL
                                                                   -----DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNL
                                                                                                                         IIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
                                                                                                                                                                                                        308 LFTMILDTFSICVTVVVLNVHFRSPQTHTMSPWVRRVFIHVLPRLLVMRRP-----
                                                                                                                                                                                                                                                                -----PHRSRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91092263; PubMed-1702381;
Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
Darlison M.G., Sattelle D.B., Barnard B.A.;
Sequence and functional expression of a single alpha subunit of an
insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398(1990).

-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXPENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-Li chain precursor.
Schistocerca gregaria (Desert locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
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InterPro; IPR006029; Neu_channel_memb.
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P23414;
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                                     PRINTS; PR00252; NRIONCHANNEL.
TIGREMAS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTE ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 EKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
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                                                                                                                           ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        74;
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N-LINKED (GLCNAC...
ALA/SER-RICH.
HIS-RICH.
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Pred. No. 1.4e-53;
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IPR006201; Neur_channel.
            Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                             Transmembrane; Multigene family SIGNAL 1 23
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ID ACH2_HUMAN STANDARD;
AC 01582; 09HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
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36.8%;
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557 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Blechschmidt K., Rosenthal A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBJUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                               TISSUE-Hypothalamus;
MEDLINE-97062879; PubMed-8906617;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                            Euteleostomi;
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. GO; GO:0007868; P:signal transduction; TAS. GO:0007168; P:synaptic transmission; TAS. InterPro; IPR0066029; Neu_channel_memb.
InterPro; IPR006502; Neu_channel_memb.
InterPro; IPR006501; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF03931; Neur_chan_memb; 1.
Pfam; PF03931; Neur_chan_memb; 1.
TIGRPAMS; TIGR00860; LIC; 1.
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Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                              Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR.
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POTENTIAL.
CYTOPLASMIC.
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EMBL; Y16281; CAA76154.1; -.
EMBL; AF311103; -; NOT_ANNOTATED_CDS.
GGNEW; HONC:1956; CHRNA2.
MIM; 118502; -.
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289
315
315
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521
                                                            Homo sapiens (Human)
                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                       366 LEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCL
                                                                                                                                                                                                                                                                                                                                                                               426 YVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 ELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 ALLQEGELLLSPH------MOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 ELKERSSKSLLANVLDIDDDFRHNCR-PMTPG-GTLPHNPAFYRTVYGQGDDGSIGPIGS
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                                                                                                                                                                                                                               Gaps
               ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

A -> I (IN REF. 3).

A -> I (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH3_HUMAN STANDARD; PRT; 503 AA.
P32297; Q15623; Q96RH3; Q99553; Q9BQ93;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
                                                                                                                                                                                                                             75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fornasari D., Chini B., Tarroni P., Clementi F.; "Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      Length
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                      21.0%; Score 848.5; DB 1; 36.7%; Pred. No. 6.6e-52;
                                                                                                                                                                                                                           87; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
  SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurosci. Lett. 111:351-356(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744 LCLIIFTMFAILATIAVLL 762
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                                                        79 N-
129 N-
235 N-
125 A-
59735 MW;
                                                                                                                                                                                    Query Match 21.0
Best Local Similarity 36.7
Matches 183; Conservative
                                                          79
129
235
125
529 AA;
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DISULFID
                                                                                                                                             SEQUENCE
                                                            CARBOHYD
                                                                                  CARBOHYD
                                                                                                   CARBOHYD
                                                                                                                       CONFLICT
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                               FEBS Lett. 400:309-314(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 6-493 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR MIM; 118503; -. Table Colored Color
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
MALAV -> MGSGPL (in isoform 2).
/FTId=VSP_000073.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P32297-2; Sequence=VSP_000073;
                                                                                                                                                                                                                                                                                                                                                 IsoId=P32297-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M30303, AAN5942.1;
EMBL, M6243; AAB40110.1;
EMBL, V08418; CAA69695.1;
EMBL, AJ007783; CAA07682.1;
EMBL, AJ007784; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, BC001642; AAH01542.1;
EMBL, BC001642; AAH01596.1;
EMBL, BC000533; AAH0296.1;
EMBL, R000534; AAH00513.1;
EMBL, M788584; AAR68110.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC002996; AAH02996.1; --
EMBL; BC000513; AAH00513.1; --
EMBL; AF385584; AAK68110.1; --
EMBL; X53559; CAA37625.1; --
PIR; A37040; A37040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M86383; AAC84176.1; -.
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RA Amentides P.C., Scherer S.E., It's P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.C., Scherer S.E., It's P.W., Hoskins R.A., Galle R.F.,
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RA Brandon R.C., Baxter E.C., Hell C., Change M., Pfelifer B.D.,
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Rount S.M., Nelson K.A., Musskern D.R., Parle Son D.R.,
Ra Allosh R., Nelson K.A., Winskern D.R., Parle Son D.R.,
Rount S.M., Nelson K.A., Winsskern D.R., Parle Son D.R.,
Rount S.M., Nelson K.A., Worley K.D. C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
Williams S.M., Woodage T., Wonley K.D. C., Scheeler F., Shen B.,
Rabe B.C., Slong F.W., Rubin G.M., Wenter E., Wang S.,
Williams S.M., Woodage T., Wolley K.D. C., Scheeler F., Shen B.,
Rabe B.C., Slong F.W., Rubin G.M., Wenter J.C.,
Rabe Bronnes Raparene D.R., Wang S., Rabe B.C., Stabone B.C., Stabone F.W., Rubin G.M., Wenter J.C.,
Rabe Bronnes Requence of Droso
                                                                                                                                                                                                                  [3] SEQUENCE FROM N.A.
MEDLINE-90360975; PubMed-1697262;
Sawruk E., Schloss P., Betz H., Schmitt B.;
Sawruk E., Schloss P., Betz H., Schmitt B.;
"Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
"Heterogeneity of prosophila nicotinic acetylcholine receptors: SAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN BETKELLEY; TISSUE-Head; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Change M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DbBJ databases.

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                                                                                         Jonas P., Baumann A., Merz B., Gundelfinger E.D.; "Structure and developmental expression of the D alpha 2 gene encoding a novel nicotinic acetylcholine receptor protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                  MEDLINE-90353591; PubMed=2117557;
                                                                                                                                                                                         FEBS Lett. 269:264-268(1990).
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                                                                                                                                                                   Drosophila melanogaster.
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                                               TISSUE-Head
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		/ 747 IIFTMFAILATIAVLLSAPH1 767 	ACH3_DROME STANDARD; PRT; 521 AA.  ID ACH3_DROME STANDARD; PRT; 521 AA.  AC P0475; 09VZC3;  DT 13-AUG-1987 (Rel. 05, Last sequence update)  DT 13-AUG-1987 (Rel. 05, Last sequence update)  DT 15-SEP-2003 (Rel. 42, Last annotation update)  ACETYICHOLINE receptor protein, beta-like chain 1 precursor.  GN NACR-BETA-64B OR ACRO OR ARD OR ACR64B OR CG11348/CG12606.  DATE OF THE OFFICE OFFIC			Wadsworth S.C., Rosenthal L.S., Kammermeyer K.L., Potter M.B., A Nelson D.J.; Nelson D.J.; Inspression of a Drosophila melanogaster acetylcholine receptor- related gene in the central nervous system."; Mol. Cell. Biol. 8:778-785(1988). SEQUENCE FROM N.A. STRAIN-BERKELEY; STRAIN-BERKELEY;	RA MEDLINE-ZOLINGUOUS, PUDMEDGE-10731132;  RA Admans M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  R George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  RA George R.A., Lewis S.E., Rachardel M.D., Zhang Q., Chen L.X.,  RA George R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D.,  RA Abrill J.E., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,  RA Abrill J.E., Baxendale J., Bayraktaroglu L., Beasley E.M.,  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  RA Berson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  RA Dodson K., Doup L.E., Downes M., Dugan-Rochas S., Dunkov B.C., Dunn P.,  RA Dodson K., Bvangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,  RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
qq	QY Db QY Db	Qy	A C C C C C C C C C C C C C C C C C C C	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	RA R RA R R R R R R R R R R R R R R R R	RA RE	X
-!- DEVELOPMENTAL STAGE: LATE EMBRYONIC -!- SIMILARITY: BELONGS TO THE LIGAND-GA	This This betw the use modi		DR F1485 5116/9; ACFFA2.  DR F1485 5116/9; ACFFA2.  DR InterPro; IPR006029; Neu_channel_memb.  DR InterPro; IPR006202; Neu_channel_memb.  DR InterPro; IPR006201; Neur_chan_LBD.  DR Pfam; PF02931; Neur_chan_memb; 1.  DR PRINTS; PR00252; NRIOWCHANNEL.  DR PRINTS; PR00252; NRIOWCHANNEL.  DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.  KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;  KW Promomorphysion. Multicone femalium.		CARBOHYD 65 65 CARBOHYD 254 254 CARBOHYD 570 570 SEQUENCE 576 AA; 65506 MW; Query Match 20.9%; Best Local Similarity 34.4%; Matches 193; Conservative 87		OY 405 DECEDGIYOTUVVNINGSCLYVPPGIFKSTCKIDITWFPPDDORCEMKFGSWTYDGFOL 464  138 DGEYVYTEMTRAILHYTGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFWKFGSWTYDGDOI 197  465 DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAII 515  198 DLKHISQKNDKDNKVEIGIDLREYYPSVEWDILGVPAERHEKYYPCCAEPYPDIFFNITL 257  OY 516 RRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETWPAT 575

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|RFSGLVGALGGGLSTLSGYNGLPSV 469
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skins R.A., Galle R.F.,
hang Q., Chen L.X.,
champ Q., Chen L.X.,
champe M., Pfeiffer B.D.,
Nelson C.R., Miklos G.L.G.,
Pfannkoch C., Baldwin D.,
taroglu L., Beasley E.M.,
dari D., Bolshakov S.,
E., Center A., Chandra I.,
E., Center A., Chandra I.,
E., Dew I., Dietz S.M.,
D., Dew I., Dietz S.M.,
ha S., Dunkov B.C., Dunn P.,
Ferriera S., Fleischmann M.,
bart W.M., Glasser K.,
uan P., Harris M.,
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iic acetylcholine receptor
ir.";
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hain 1 precursor.
G11348/CG12606.
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la.";
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

A Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,

Kanimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Mattei B., McIntosh T.C., McIeod M.P., McPherson D.,

Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Randson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,

Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Randson D.K., Siden Krämos I., Simpson M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Rands Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Randson R.M., Robin G.M., Venter J.C.;

Stables R.A., Myers E.W., Rubin G.M., Venter J.C.;

Schence 287:185-2195(2000).

C. !- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

ELEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: CNS IN EMBRYOS.
-i- DEVELOPMENTAL STAGE: LATE EMBRYONIC AND LATE PUPAL STAGES.
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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FF9BA2ABC0C3AA62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
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FlyBase; FBgn0000038; nAcR-beta-64B.
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Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransmembrane; Multigene family
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323
481
500
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TRANSMEM
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Length 521;

Score 840; DB 1; Pred. No. 2.6e-51;

20.8%;

Local Similarity

Match

Query Best L

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6
                                     291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID 350
                                                                                                                 410
                                                                                                                                     469
                                                                                                                                                                                                                   365
                                                                                                                                                                                                                                                                         470 DETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEP-YIDITFAIIIRRRILYYFFNLII 528
                                                                                                                                                                                                                                                                                                                                                                                              305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL-- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GLGD----GCRRESESSDSILLSPEASKATE-----AVEFIAEHLRNE 462
                                                           351 VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                               411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQL-Q
                                                                                                                                                                                                                                                                                               306 TFIMNIVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLFMKRPRKTRLRWMMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612 PCSDTSSERKHQILSDVELKERSS----KSLLANVLDIDDDFRHNC---RPMTPGGTLPH
                                                                                                                                                                                                                                                                                                                                                       529 PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THREE NON-ALPHA CHAINS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 11, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.; "Genese expressed in the brain define three distinct neuronal nicotinic acetylouline receptors."; EMBO J. 7:595-601(1988).
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI 767
Mismatches 172;
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95;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus.
NCBI_TaxID=9031;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 FVTLSIIITVFVLNVHHRSPSTHTMPHWVRSFFLGFIPRWLFMKRP--PLLLPAEGTTGQ 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EFPTTPC-----SDTSSERKHQILSDVELKERSSKSLLANVL---DIDDDDFRHN 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||: ::| | || || ||:|:| ::|||||||| || LISCLIVLVFYLPSDCGEKITLCISVLLSLIYFLLITEIIPSTSLVIPLIGEYLLFTMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
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                                                                                                                                                                                                                                                                                                                                  NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-2 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

E76C6360AF876364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                            PROSITE; PS00236; NEUROTK_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.6e-51;
81; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                     PIR, S00377; ACCH2N.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NEUR_CHANNEL.
TIGRFAMS; TIGR00860; LIC; ILC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%; Score 838;
                                                                                          EMBL; X07340; CAB59645.1; JOINED.
EMBL; X07341; CAB59645.1; JOINED.
EMBL; X07342; CAB59645.1; JOINED.
EMBL; X07344; CAB59645.1; JOINED.
EMBL; X07344; CAB59645.1; JOINED.
EMBL; AJ250360; CAB59625.1; -
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                                                                               EMBL; X07339; CAB59645.1; -
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290
327
501
520
172
223
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104
528 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
653 CRPM---TPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGL 709
                                     467
                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-44.
MEDLINE-85270494; PubMed-3860855;
Conti-Troncooli B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
Ray N., Raftery M.A.;
"Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87144271; PubMed-3821734;
Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P.;
Klarsfeld A., Daubas P., Hourachot B., Changeux J.-P.;
As 5'-flanking region of the chicken acetylcholine receptor alpha-
subunit gene confers tissue specificity and developmental control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                 DELTA, AND GAMMA CHAINS.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE OF 180-227 AND 260-333 FROM N.A.
MEDLINE-84206570; PubMed-6337170;
Ballivet M., Nef P., Stalder R., Fulpius B.;
Genomic sequences encoding the alpha-subunit of acetylcholine receptor are conserved in evolution.";
Cold Spring Harb. Symp. Quant. Biol. 48:83-87(1983).
                                                                              710 ILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.; "Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors.";
                                       431 CERQAGKASGGPAPQVPLKGEEV---GSDQ-----GLTLSPSILR---
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                                                                                                                                                                                                                    456
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MEDLINE=88283624; PubMed=3267226;
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EMBL; X07331; CAA30282.1; JOINED
EMBL; X12434; CAA30282.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression in transfected cells. Mol. Cell. Biol. 7:951-955(1987)
                                                                                                                                                                                                                                                       (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-12 FROM N.A.
                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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P09479;
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293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD 352
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TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; SIGNAL.
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                                                                                                                                                                                                                                                                                              ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION.
N-LINKED (GLCNAC. . ) (PROBABLE).
E -> D (IN REF. 4).
0B31B6EABD7B4b42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.5%; Score 827.5; DB 1; Length 456; 34.6%; Pred. No. 1.6e-50; ive 92; Mismatches 130; Indels 111;
                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
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416 DEWKFVAMVLDHLLLVIFMLVCIIGTLAV 444
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; I.
Pfam; PF02932; Neur_chan_memb; 1.
X07335; CAA30282.1; JOINED. AJ250359; CAB59624.1; -. AF051909; AAC06012.1; -.
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52183 MW;
                                              EMBL; M14808; AAA48565.1; -. EMBL; M14809; AAA48564.1; -. PIR; I50150; I50150.
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Matches 176; Conservative
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456 AA;
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Search completed: August 13, 2003, 15:26:10 Job time: 19.1234 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 13, 2003, 15:21:45; Search time 28.7606 Seconds (without alignments) 2574.698 Million cell updates/sec

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB.seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	nicotinic acetylch			alpha-bungarotoxin	nicotinic acetylch	alpha 7 neuronal n	nicotinic acetylch	hypothetical prote			O)		nicotinic acetylch						nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch							
SUMMARIES	ID	A57175	JN0113	T01378	JH0173	ACHUA7	G02259	868588	T25671	T19622	T19862	ACFFA1	S12359	A53956	ACFFA2	ACFFNN .	A37040	ACCH2N	A40110	ACCHAN	A24572	860589	B37014	T09289	S12899	G02421	ACHUA1	ACBOA1	A28529	A24383
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	Length	502	505	505	511	502	502	498	461	260	542	267	557	503	576	521	203	528	511	456	499	495	512	464	200	498	.457	457	457	457
de	Ouery	29.5	29.5	29.0	28.9	28.7	28.6	27,3	25.0	24.4	24.0	22.0	21.6	20.9	20.9	20.8	20.8	20.7	20.2	20.5	20.4	20.3	20.3						19.7	19.6
	Score	1182.5	1179.5	1173.5	1168	1160.5	1155.5	1104	1009.5	86	968.5	883	873	845	843.5	841	840	838	828	827.5	$\sim$	820.5	820.5	81	806.5	805	802.5	$\sim$	794.5	794
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	acerytcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	protein F25G6.4 [i	nicotinic acetylch	nicotinic acetylch	hypothetical prote	nicotinic acetylch	nicotinic acetylch	hypothetical prote
. (	149458	S13872	A39218	ACCHIN	JH0174	I50548	B35721	S10505	JC4021	E89134	ACCH4N	ACRYA1	T24724	A26456	S08162	T23843
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	440	457	470	491	503	461	495	502	627	559	622	461	468	625	457	265
(	13.0	19.5	19.5	19.5	19.4	19.4	19.3	19.3	19.3	19.3	19.3	19.3	19.2	19.2	19.1	19.1
(	196.5	789	789	787	.785	783	782	782	780	779.5	779.5	779	176	775.5	773.5	773
ć	2	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1	
AS/1/5	85/1/3 ninchinic acetulcholine recentor alpha-7 chain precursor, neuropal - mouse
C:Species: Mus	
C; Date: 05-Ja	C.Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C; Accession: A57175	357175
R;Orr-Urtrege	c, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
Genomics 26,	Genomics 26, 399-402, 1995 Genomics 26, 399-402, 1995 Genomics 26, 399-402, 1995
A; IICIE: CIOII	tilg attu mapping of the mouse affilia", herioliai incottinic acetylchoffine fec imbar af717f. Mitth 65.27403f. DMTh.7760147A
A; Accession:	15/1/5
A; Status: preliminary	liminary
A; Molecule type: mRNA	De: MRNA
A; Residues: 1	-502 <orr></orr>
A; Cross-refer	ences: GB:137663; NID:9790853; PIDN:AAC42053.1; PID:9790854
C; Superiamity	Superiaminity: acetylcholine fecepton Sourcests brain aluconactain for channel neurotranemitter recentor, phosphonrote
E:1-23/Domain	tain; giyoopiotein; ion channei; neutotiansmirtei tedeptoi; phosphopiote : signal seguence #status predicted <sig></sig>
F; 24 - 502/Prodi	24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F; 231-254/Dom	in: transmembrane #status predicted <trl></trl>
F; 262-280/Dom	in: transmembrane #status predicted <tr2></tr2>
F; 296-317/Dom:	F:296-317/Domain: transmembrane #status predicted <tr3></tr3>
E;4/0-400/DOME	111: Lanishemblade #Steure bledicted virk. 131: Lanishemblade #Steure bledicted virk.
F: 46, 50, 133/B	40,70,70,70mining Site: calbonylmate (Ash) (Covalent) #status predicted 40,70,70 pinding site: bhosphate (Ser) (Covalent) #status predicted
F, 415/Binding	F,415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding	site: pnospnate (Tyr) (covalent) #status predicted
Query Match	29.2%; Score 1182.5; DB 2; Length 502;
Matches 23	Best Local Similarity 43.8%; Fred. NO. 3.16-77; Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;
Qy 297	
Db 8	:  :  :  :  :  :  :  :  :  :  :  :  :
Qy 354	KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
Db 68	:  :  :  :
Qy 414	
Db 128	THVLVNASGHCQYLPPGIFKSSCYIDVRWFPFDVQQCKLKFGSWSYGGWSLDLQMQE 184
Qy 474	
Db 185	ADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTYTVTMRRRTLYYGLNLLIPCVLI 244
Qy 534 /	ASMALLGETLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581
Db 245	:::             :   :          SALALLVFLPADSGEKISLGITVLLSLTVFLLVADSGEKISLGITVLLVALLVADSGEKISLGITVLLVALLVALIAQYFASTMIIV 304

ON 562	Ouery Match  Query Match  Best Local Similarity 45.7%; Pre  Matches 237; Conservative 80;  Qy 295 LLIYLNLSAKVCLAGYHEKR	Oy 472 Oy 472 Oy 632 Oy 532 Oy 532 Oy 532 Oy 582 all Db 303 Oy 615	DD 358 QHKQKKCSL5SMEMNIVSGQQ QY 670 RTVYGQGDDGSIGPIGSTRMPDA 407GRMTCSPTEEE QY 730 IANDWKEAAMVVDRLCLIFFTWE DD 456 ICNEWKEAAAVVDRLCLIFFTWE DD 456 ICNEWKEAASVVDRLCLIFFTWE	Promoter de nicotain receptor alpha 7 chain - ra rolaise nicotain receptor alpha 7 chain - ra cispecies: Rattus norvedicus (Norway C.Date: 12-Feb-1999 #sequence_revisio C.Accession: T01378 R.Seguela, P.; Wadiche, J.; Dineley-M R.Seguela, P.; Wadiche, J.; Dineley-M R.Seguela, P.; Madiche, J.; Dineley-M A.Seguela, P.; P. Seguela, P.; P.; P. Seguela, P.;	od in
	582	RESULT 2 JN0113 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken N.Alternate names: alpha-bungarotoxin-binding protein alpha chain C;Species: Gallus gallus (chicken) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999 C;Accession: JN0113; JH0172; S28018; B25738; S26566 R;Coutunier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Mil Neuron 5, 847-856, 1990 A;Fitle: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is devel A;Reference number: JN0113; MuID:91097796; PMID:1702646 A;Recession: JN0113 A;Molecule type: DNA A;Residues: 1-502 <c0005050< td=""><td>A;CrossTreterences: GB:Xb8308, NLD:g247/55; FIDN:CAA485/6.1; FID:g28//5/ A;Experimental source: white leghorn; brain R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron:5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtype A;Reference number: JH0172; MUID:90315158; PMID:2369519 A;Molecule type: MRNA A;Residues: 1-502 <sch> A;Cross-son: JH0172 A;Cross-son: JH01</sch></td><td>Rymatter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J. Bay atter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J. Band J. 11, 4529-4538, 1992 A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor pi A; Reference number: \$28018; MUID:93049204; PMID:142587 A; Accession: \$28018; MUID:93049204; PMID:142587 A; Rocession: \$28018; MUID:93049204; PMID:142587 A; Rosidues: 1-18 cAma&gt; A; Rosidues: 1-18 cAma&gt; A; Rosidues: 1-18 cAma&gt; A; Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, B.A.; Dolly, J.O.; Lai, F.A.; Re Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985 A; Title: Brain and muscle nicotinic acetylcholine receptors are different but P A; Reference number: A4055; MUID:85270494; PMID:3860855 A; Accession: B25738 A; Molecule type: protein A; Residues: 24-25, ET', 28-41, 'X', 43-45, 'X', 47 cCON&gt; C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is</td><td>Gigenetics:  A; Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3 C; Superfamily: acetylcholine receptor C; Keywords: brain: glycoprotein; ion channel; neurotransmitter receptor; phospl F; 1-23/Domain: signal sequence #status predicted <sig>F; 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #state; F; 231-254/Domain: transmembrane #status predicted <tr1>F; 24-500/Domain: transmembrane #status predicted <tr2>F; 26-317/Domain: transmembrane #status predicted <tr3>F; 470-488/Domain: transmembrane #status predicted <tr4>F; 46-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 45-90,133/Binding site: phosphate (TR1) (covalent) #status predicted F; 415/Binding site: phosphate (TR7) (covalent) #status predicted F; 442/Binding site: phosphate (TR7) (covalent) #status predicted</tr4></tr3></tr2></tr1></sig></td></c0005050<>	A;CrossTreterences: GB:Xb8308, NLD:g247/55; FIDN:CAA485/6.1; FID:g28//5/ A;Experimental source: white leghorn; brain R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron:5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtype A;Reference number: JH0172; MUID:90315158; PMID:2369519 A;Molecule type: MRNA A;Residues: 1-502 <sch> A;Cross-son: JH0172 A;Cross-son: JH01</sch>	Rymatter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J. Bay atter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J. Band J. 11, 4529-4538, 1992 A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor pi A; Reference number: \$28018; MUID:93049204; PMID:142587 A; Accession: \$28018; MUID:93049204; PMID:142587 A; Rocession: \$28018; MUID:93049204; PMID:142587 A; Rosidues: 1-18 cAma> A; Rosidues: 1-18 cAma> A; Rosidues: 1-18 cAma> A; Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, B.A.; Dolly, J.O.; Lai, F.A.; Re Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985 A; Title: Brain and muscle nicotinic acetylcholine receptors are different but P A; Reference number: A4055; MUID:85270494; PMID:3860855 A; Accession: B25738 A; Molecule type: protein A; Residues: 24-25, ET', 28-41, 'X', 43-45, 'X', 47 cCON> C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is	Gigenetics:  A; Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3 C; Superfamily: acetylcholine receptor C; Keywords: brain: glycoprotein; ion channel; neurotransmitter receptor; phospl F; 1-23/Domain: signal sequence #status predicted <sig>F; 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #state; F; 231-254/Domain: transmembrane #status predicted <tr1>F; 24-500/Domain: transmembrane #status predicted <tr2>F; 26-317/Domain: transmembrane #status predicted <tr3>F; 470-488/Domain: transmembrane #status predicted <tr4>F; 46-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 45-90,133/Binding site: phosphate (TR1) (covalent) #status predicted F; 415/Binding site: phosphate (TR7) (covalent) #status predicted F; 442/Binding site: phosphate (TR7) (covalent) #status predicted</tr4></tr3></tr2></tr1></sig>

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nal properties, and distribution of rat brain alph 147931; PMID:7678857
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LYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDE 67
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ion 12-Feb-1999 #text_change 21-Jul-2000
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                                                                           (SLL-ANVLDIDDDFRH----NCRPMTPGGTLPHNPAFY
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red. No. 2.2e-76;
Mismatches 119; Indels 85; Gaps
 ore 1179.5; DB 2; Length 502;
ed. No. 8.3e-77;
Mismatches 127; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller, K.; Dani, J.A.; Patrick, J.W.
Length 502;
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	Db 187 DLQMLEADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLLYGL 243  Qy 525 NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581  [1:1 1 1 ::  1  1  ::  1  1   :  1
Qy 727 CNDIANDWKFAAMYVDRLCLIIFTWFAILATIAVLLSAPHII 768   ::	RESULT 5 ACHUA7 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human N;Alternate names: cholinergic nicotinate receptor alpha-7 chain
RESULT 4 JH0173 alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken C:Species: Gallus gallus (chicken) C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 C:Accession: JH0173 R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein CDNAs and MAbs reveal subtypes of this A;Reference number: JH0172; MUID:90315158; PMID:3369519	C; Species: Homo saplens (man) C; Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999 C; Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999 C; Accession: 137185; A54194; S60309 R; Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J. Mol. Pharmacol. 45, 546-554, 1994 A; Title: Human alpha 7 acctylcholine receptor: cloning of the alpha 7 subunit from th omers expressed in Aenopus cocytes. A; Reference number: 137185; MUID: 94195283; PMID: 8145738 A; Accession: 137185 A; Accession: Lanslated from GB/EMBL/DDBJ A; Molecule type: mRNA
A,Accession: JH0173 A,Molecule type: mRNA A,Molecule type: mRNA A,Molecule type: mRNA A,Molecule type: mRNA A,Mossiues: 1-511 <sch> A,Estalues: 1-511 <sch> A,Experimental source: brain A,Mote: this sequence is similar to acetylcholine receptor alpha chains C,Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend C,Superfamily: acetylcholine receptor</sch></sch>	A;Residues: 1-502 <pen> A;Cross-references: EMBL:X70297; NID:9496606; PIDN:CAA49778.1; PID:9496607 A;Experimental source: brain neuroblastoma cell line SHSY-5Y R;Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S. Genomics 19, 379-381, 1994 A;Ttle: Wolecular cloning and chromosomal localization of the human alpha-7-nicotini A;Reference number: A54194; MUID:94245214; PMID:8188270 A;Accession: A54194</pen>
C; Keywords: glycoprotein; transmembrane protein F;1-30/Domain: signal sequence #status predicted <sig> F;1-30/Domain: signal sequence #status predicted <sig> F;239-262/Domain: transmembrane #status predicted <tm1> F;239-262/Domain: transmembrane #status predicted <tm3> F;30-283/Domain: transmembrane #status predicted <tm3> F;30-283/Domain: transmembrane #status predicted <tm3> F;30-0000 in transmembrane #status predicted <tm3> F;30-0000 in transmembrane #status predicted <tm4> F;479-496/Domain: transmembrane #status predicted <tm4> F;54/Binding site: carbohydrate (Asn) (covalent) #status predicted</tm4></tm4></tm3></tm3></tm3></tm3></tm1></sig></sig>	A; Molecule type; mRNA A; Molecule type; mRNA A; Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <chi> A; Cross-references: GB: 223141; NID: 9457736; PIDN: CAA80672.1; PID: 9457737 A; Experimental source: retina C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali C; Genetics: A; Gene: GDB: CHRNA7 A; Cross-references: GDB: 138751; OMIM: 118511</chi>
Query Match 28.9%; Score 1168; DB 2; Length 511; Best Local Similarity 44.2%; Pred. No. 5.7e-76; Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;  Qy 285 NGLNKHSWIFLLIYLNLSARVCLAGYHEKRLHDLLDPYWTLERPVLNESDPLQLSFGLT 344  11 :	A; Map position: 13q14-13q14 A; Note: defects in this gene have been associated with mental retardation and schizop C; Complex: the functional receptor molecule is a heteropentamer with two alpha chains C; Superfamily: acetylcholine receptor C; Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept F; 1-23/Domain: signal sequence #status predicted <sig> F; 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr F; 231-254/Domain: transmembrane #status predicted <tr1></tr1></sig>
Qy 345 LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404  :	F;267-280/Domain: transmembrane #status predicted <tr2> F;296-317/Domain: transmembrane #status predicted <tr3> F;470-488/Domain: transmembrane #status predicted <tr4> F;46.90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F;150-164/Disulfide bonds: #status predicted</tr4></tr3></tr2>
405 127 465	F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted F;415/Binding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Tyr) (covalent) #status predicted Onery Match
DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF     : :     :	Query Match 28.7%; Score 1100.5; DB 1; Length 502; Best Local Similarity 45.1%; Pred. No. 1.9e-75;

Db 185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYG	Oy 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETMPATSDAVPL 1::	Oy 582RI  Db 305 GLSVVYTVIVLQYHHDDPGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRI	Qy 613 CSDTSSERHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG	Qy 669 YRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKE:	Qy 724 DDECNDIANDWRFAAMWVDRLCLIIFTMFAILATIAVLLSAPHII 768     ::	RESULT 7 S68588 nicotinic acetylcholine receptor alpha-1 chain precursor (clone C.Species: Caenorhabditis elegans C;Date: 06-Dec-1996 *sequence_revision 07-Feb-1997 *text_change C;Accession: S68588; S57496	R.Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D. J. Mol. Biol. 258, 261-269, 1996 A;Title: Nicotinic acetylcholine receptors in the nematode Caeno A;Reference number: S68587; MUID:96196478; PMID:8627624	A; Accession: S08588 A; Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1.498 < RBL: A; Cross-references: EMBL: X83887; NID: 9872087; PIDN: CAA58764.1; P.	C;Superfamily: acetylcholine receptor C;Keywords: qlycoprotein; ion channel; neurotransmitter receptor F;1-19/Domain: signal sequence *status predicted <sig>F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain</sig>	Query Match 27.3%; Score 1104; DB 2; Length 498 Best Local Similarity 43.3%; Pred. No: 2.1e-71; Matches 227; Conservative 76; Mismatches 139; Indels	Qy 295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT:	Qy 355 NOLLYTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 	QY 415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL  :: : : :  :	Qy 475 -DISSYVENGEWELLGVPCKRNETYYNCCPEPYIDITFAIIIRRTLYYF	Qy 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL	QY 582	Qy 617 SSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPM : :
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;	297 IYLNLSAKVCLAGYHEKRLLHDLIDPYNTLERPVINESDPLQLSFGLTLMQIIDVDE 353 ::   :           ::	354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIMKPDVLMYNSADEGFDGTYQ 413 	414 TNVVVRNNGSCLXVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473     :  :	474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533 	534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL581 :::	582	669 YRTVYGGGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRK 723   1	724 DDECNDIANDWKFAAMVVDRLCLIIFTMFALLATIAVLLSAPHII 768 	RESULT 6 G02259 alpha 7 neuronal nicotinic acetylcholine receptor – human	ecies: Homo sapiens (man) ite: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 :cession: G02259 sonard, S.	submitted to the EMBL Data Library, November 1995 A;Reference number: H00936 A;Accession: G02259 A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Molectife (Type: micha A;Residues: 1-502 <led> A;Gross references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077 C;Superfamily: acetylcholine receptor</led>	Ouery Match Best Local Similarity 45.1%; Pred. No. 4.4e-75; Matches 237; Conservative 80; Mismatches 117; Indels 91; Gaps 12;	297 IYLNLSAKVCLAGYHEKRLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353 ::   :	354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413	414 TNVVYNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473    :  :  :  :  :  :  :  :  :  :  :  :	474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533

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KVALQQIIDVDEK 65
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KKLD--LQPATGG 183
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VRP-ACQHKQRR 363
KGLNLLIPCVLI 244
                                       RANTERSTMIIV 304
                                                          RPLILEFPTTP 612
                                                                                                 PEGTLPHNPAF 668
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RESULT

JOY FGTANKING TOSTONMENTKPKNPL
659 GGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFIT

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hypotherical protein C31H5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Ta-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19622
R;Kershaw, J.
Submitted to the EMBL Data Library, April 1997
A;Reference number: Z19153
A;Reference number: Z19153
A;Reference number: Z19153
A;Reference number: L19622
A;Retus: prelliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-560 <WILL>
A;Residues: 1-560 <WILL>
A;Residues: CSPC-C31H5.3
A;Residues: CSPC-C31H5.3
A;Reperimental source: clone C31H5
C;Genetics: A;App position: Z34/I: 70/3; 139/2; 270/I; 299/I; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 QGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW 734
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 QTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 GGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 24.4%; Score 988; DB 2; Length 560;
Best Local Similarity 37.2%; Pred. No. 5.3e-63;
Matches 214; Conservative 85; Mismatches 152; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                614 SDTSSERKHQ-----IL----
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A;Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A;Note: 538-Tyr was also found
C;Genetics:
A;Genetics:

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nicotinic acetylcholine receptor alpha-Ll chain precursor - desert locust
nicotinic acetylcholine receptor alpha-Ll chain precursor - desert locust
C; Species: Schistocerca gregaria (desert locust)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C; Accession: S12358
Accession: S12358
EMBO J. 9, 4391-4398, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 VTIMTKAILHHTGKVVWKPPAIYKSFCEIDVEYFPFDEQTCFMKFGSWTYDGYMVDLRHL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 LGKYLLFTMMLVTLSVVVTIAVLNVNFRSPVTHRMAPWVQRLFIQILPKLLCIERPKK-- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EEPEEDQPPEVLTDVYHLPP------DVDKFVNYDSKRFSGDYGIP 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 SWIFLLIYLNLS-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 DVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 YFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 ILEFPTTPCSDTSSERKHQILSDV-ELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.0%; Score 889; DB 1; Length 567
35.2%; Pred. No. 6.7e-56;
.ive 91; Mismatches 168; Indels
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Matches 196; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                  A;Gene: CESP:C40C9.2
A;Map position: X
A:Introns: 11/3: 69/3: 123/2: 173/3: 216/1: 248/1: 279/1: 314/1: 350/3: 430/1: 464/1:
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQ------DETGGDISSYVLN 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 VVFTVLVLNLHNRKPETHEMSPFLRELLLIWLPWLLLMRRPGKTIF-----NCTHLKAE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKHQILSDVELKE------RSSKSLLANV-----LDIDDDF--RHN-CRPM 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 TPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEY-----ELGLI 710
                                                                                             A; Accession: T19862
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-542 <WIL>
A; Resirences: EMBL: 270266; PIDN: CAA94206.1; GSPDB:GN00028; CESP: C40C9.2
A; Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDM 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711 LKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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A; Molecule type: DNA
A; Residues: 1-567 < BOS>
A; Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A; Rocession: A38801
A; Molecule type: mRNA
A; Residues: 1-567 < BOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 968.5; DB 2;
Pred. No. 1.3e-61;
                                          Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%; SCO
38.7%; Pre
tive 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 208; Conservative
         R;Hembry, C.
submitted to the EMBL Data
A;Reference number: 219188
A;Accession: T19862
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submitted to the EMBL Data Library, June 1990
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                                                      A, Description: Nucleotide s
A, Reference number: S21338
A, Accession: S21338
                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 30-503 <ANA>
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Best Local Similarity
Matches 178; Conserv
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A; Title: Sequence and functional expression of a single alpha subunit of an insect nicot A; Reference number: $12359; MUID:9109263; PMID:1702381
A; Accession: $12359
A; Accession: $12359
A; Accession: $12359
A; MUID:9109263; PMID:1702381
A; Cross-references: EMBL:X55439; NID:910133; PIDN:CAA39081.1; PID:910134
A; Cross-references: EMBL:X55439; NID:910133; PIDN:CAA39081.1; PID:910134
C; Superfamily: acetylcholine receptor
C; Superfamily: acetylcholine receptor alpha-Li chain #status predicted ASIC>
F: 24-557/Product: nicotinic acetylcholine receptor alpha-Li chain #status predicted AMI
F: 245-266/Domain: transmembrane #status predicted AMI>
F: 308-329/Domain: transmembrane #status predicted AMI>
F: 501-523/Domain: transmembrane #status predicted AM
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C;Date: O'Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A55956; S21338
R;Mihovilovic, M.; Roses, A.D.
R;Mihovilovic, M.; Roses, A.D.
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A53956
A;Accession
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Matches 197; Conservative
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nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila mela
sequence of the mature human nicotinic acetylcholine recept
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EMBO J. 9, 2671-2677, 1990
A;Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel
A;Reference number: S11679; WUID:90360975; PMID:1697262
A;Recession: S11679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                      A;Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:
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A;Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A;Note: 232-11e was also found
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35.2%; Pred. No. 8.2e-53;
iive 97; Mismatches 166;
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Nucleic Acids Res. 18, 3640, 1990
                                                                                                                                                                                                   A;Gene: GDB:CHRNA3
A;Cross-references: GDB:125219; OMIM:118503
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C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
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A;Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acety A;Reference number: S10306; MUID:90301489; PMID:2114015 A;Accession: S10306 A;Accession: S10306 A;Molecule type: mRNA A;Residues: 1-576 < ABAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: FlyBase:nAcR-alpha-96Ab
A;Cross-references: FlyBase:FBgn000039
A;Gene: FlyBase:nAcR-alpha-96Ab
A;Cross-references: FlyBase:FBgn000039
A;Map position: 38 96A
A;Map position: 38 96A
A;Map position: 38 96A
A;Map position: 38 96A
A;Map position: 84/3: 136/2; 196/3; 250/1; 445/2; 512/3
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;141-256/Froduct: nicotinic acetylcholine receptor alpha-2 chain #status predicted <SXT>
F;26-280/Domain: transmembrane #status predicted <TM1>
F;237-348/Domain: intransmembrane #status predicted <TM3>
F;349-256/Domain: intransmembrane #status predicted <TM3>
F;357-345/Domain: transmembrane #status predicted <TM3>
F;557-445/Domain: transmembrane #status predicted <TM4>
F;65,254,570/Aniding site: carbohydrate (Asn) (covalent) #status predicted
F;169-183/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel A;Reference number: S11084; MUID:90353591; PMID:2117557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DL----QLQD-----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 DLKHISQKNDKDNKVEIGIDLREYYPSVEWDILGVPAERHEKYYPCCAEPYPDIFFNITL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----WIRIVFLCWLPWILRMS 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 SLALPLIGKYLLFTMLLVGLSVVITIIILNIHYRKPSTHKMRPWIRSFFIKRLPKLLLMR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKE-----RSSKSLLANVLDIDDDFRHNC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 MQMNSGSSPDSLRRMQGRVGAGGCNGMHVTTATNRFSGLVGALGGGLSTLSGYNGLPSV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 HIWRHCKPLCLLLVLLLLCETVQANPDAKRLYDDLLSNYNRLIRPVSNNTDTVLVKLGLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||:| ||||||| |: :::| | || ||||||::| ::||| |:| :::| :|:| |::| ::| |:| |::| ::| :|:| |::| |::| ::| ::| ::| ::| |::| |::| :::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| :::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
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                                                                                                                                                                                                                                          A;Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803 R;Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, E.D. FEBS Lett. 269, 264-268, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown A; Molecule type: DNA A; Residues: 42-90, 'I', 92-576 <JON>
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C; Keywords: glycoprotein; no channel; neurotransmitter receptor; postsynaptic membra F; 1-24/Domain: signal sequence #status predicted <SIG> F; 25-21/Product: nicotinic acetylcholine receptor nonalpha chain #status, predicted <F; 25-236/Domain: extracellular #status predicted <EXT> F; 25-236/Domain: transmembrane #status predicted <TML> F; 269-285/Domain: transmembrane #status predicted <TML> F; 269-285/Domain: transmembrane #status predicted <TML> F; 324-481/Domain: itransmembrane #status predicted <INT> F; 324-481/Domain: itransmembrane #status predicted <INT> F; 482-500/Domain: transmembrane #status predicted <INT> F; 482-500/Domain: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-55, (7, 77-72, 'v', 74-521 <SAW2>
R; Hearmans-Borgmeyer. I.; Zopf, D.; Ryseck, R.P.; Hovemann, B.; Betz, H.; Gundelfinger
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A; Title: Primary structure of a developmentally regulated nicotinic acetylcholine rec
A; Reference number: A26313
nicotinic acetylcholine receptor nonalpha chain precursor – fruit fly (Drosophila mel
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A; Residues: 1-72, V., 74-521 <HER>
A; Cross-references: EMBL: X04016; NID: 97537; PIDN: CAA27641.1; PID: 97538
A; Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
Mol. Cell. Biol. 8, 778-785, 1988
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A; Reference number: A28126; MUID: 88174720; PMID: 2832736
                           C; Species: Drosophila melanogaster
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C; Accession: S03012; A38044; A26313; A28126; A38759
R; Sawruk, E.; Hermans-Borgmeyer, I.; Betz, H.; Gundelfinger, E.D.
A; Title: Characterization of an invertebrate nicotinic acetylcholine receptor gene: A; Reference number: S03012; MUID:88296842; PMID:3136037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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A; Residues: 1-521 <SAW>
A; Cross-references: EMBL:X07956; NID:g7602; PIDN:CAA30778.1; PID:g1065712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 521;
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A; Introns: 22/1; 67/3; 119/2; 267/3; 467/3
C; Superfamily: acetylcholine receptor
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A.Accession: A28126
A.Molecule type: mRNA
A.Residues: 1-521 <WAD>
A.Cross-references: EMBL:M20316
C.Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           A; Accession: S03012
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IL 245	576	LF 305	rr 611	EM 365	РН 664	423	KD 724	: NE 462		
187 NKNFVDLSDYWKSGTWDIIEVPAYLN-VYEGDSNHPTETDITFYIIIRRKTLFYTVNLIL 245	529 PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETMPATS 576	246 PTVLISFLCVLVFYLPAEAGEKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLF 305	DA	306 TFIMNTVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLFMKRPRKTRLRWMMEM 365	612 PCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664	366 PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL 423	GSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILK	424GCRRESESSDSILLSPEASKATEAVEFIAEHLRNE 462	725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI 767	
187	525	246	577	306	612	366	99	424	725	463
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Search completed: August 13, 2003, 15:30:19 Job time : 30.7606 secs THIS PAGE BLANK (USPTO)

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Drosophila melanog
Neuronal alpha-bun
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/SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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    protein search, using sw model

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## AAY50814 standard; Protein; 770 AA. (first.entry) 17-FEB-2000 AAY50814;

RESULT 1 AAY50814

ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. D. melanogaster acetyl-choline receptor protein from clone Da7.

Drosophila melanogaster DE19819829-A1 11-NOV-11999. 

98DE-1019829. 98DE-1019829 04-MAY-1998; 04-MAY-1998; Schulte Adamczewski M, Oellers N,

(FARB ) BAYER AG.

WPI; 2000-014207/02. N-PSDB; AA224475.

Human neuronal nic Neuronal nicotinic

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides

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AAY50815 standard; Protein; 496
           AAY50815
RESULT
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                                  acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its requiatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified requiatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
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                          This invention describes a novel nucleic acid (NA) encoding a nicotinic
                                                                                                                                                                                                                                                                                                                                  HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 LLIYLNLSAKVCLAGYHEKRLCHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                              acetyl-choline receptor protein from clone Hva7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.8%; Score 1850; DB 21; 70.0%; Pred. No. 3.5e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1a; Page 17-19; 26pp; German
                                                                                                                                                                                                                                                                                                       98DE-1019829
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    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361; Conservative
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                                                                                                                                                               Heliothis virescens.
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                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER AG.
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                                                  virescens
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17-FEB-2000
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Best Local 3
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                                                                                                                                                                                                                                         673 YGQG-----DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD 724
65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                LLALLPVSEQ - - - - GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                               NQLLYINVWLKLEWNDWNLRWTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                            DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                                                       SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                    ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                                                                                                                                                                                                                                                 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                            NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 37938; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 37938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
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11-JUL-2000; 2000US-0614150.
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                                317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---WIRIVELCWLPWILRMSRPG---RPLILEFPTTPCS
                                                                           DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; ACHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides {}^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                              H. virescens acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.8%; Score 1609; DB 21; Length 501; 60.8%; Pred. No. 5.7e-139; 1ve 57; Mismatches 65; Indels 84
                                                                                                                                                                                                                       KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1a; Page 22-23; 26pp; German.
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                                                                                                                                                                                                                                                                                                                AAY50816 standard; Protein; 501
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 319; Conserv
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AG.

(FARB ) BAYER

DE19819829-A1

17-FEB-2000

AAY50816;

04-MAY-1998; 04-MAY-1998;

11-NOV-1999

Adamczewski M,

N-PSDB; AAZ24477

Sequence Query Match

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                                                                                                                                                                                                                                                                                                                                                                   241 LFRRIAASTIAFISYLGSFAAQLRSSSSSSSNSGNSSSTQILNGLNKHSWIFLLIYL 300
                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                   9
                                                                                                               specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
    invention
capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics of pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0178-ABL30511), and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                                         MKNAQLKLTEVDDDDELWLAVRLAHCSSNISSSSTRTTSSNKRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                                                                               HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                                                                                                                                                                                                                                                                             LFRRIAASTIAFISYLGSFAAQLKNSSSSSS-SSNSSNNSSTQILNGLNKHSWIFLLIYL
                                                                                                                                                                                                                                                                                                                                                                                                          TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
                                                                                                                                                                                                               Gaps
                                                                                               The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                  Length 327;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 17841
                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                 Pred. No. 4.4e-129;
                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                    Score 1498.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB63683 standard; Protein; 311 AA
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                                                                                                                                                                                  37.18;
97.48;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                              Matches 297; Conservative
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N-PSDB; ABL07786.
                                                                      sequences (ABL01840 (ABB57737-ABB72072)
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NLSAK 305
                                                                                                                                                         327 AA;
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                                                                                                                                                          Sequence
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                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA (ABB57737-ABB72072)
detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 LLIY --- LNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581
                                                      Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuronal alpha-bungarotoxin binding protein alphal subunit.
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                 34.8%; Score 1407.5; DB 2.88.6%; Pred. No. 9.7e-121; ive 18; Mismatches 12;
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 New isolated nucleic acid
genes from Drosophila and
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Matches 257; Conservative
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/label=
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                          interactions
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(first entry)

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alpha-bungarotoxin binding protein alpha 2; cholinergic;
                                             Weuronal alpha-bungarotoxin binding protein alpha2 subunit.
                       17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ADISGYISNGEWDLVGIPGKRTESFYECCKEPYPDITFTVTMRRTLYYGLNLLIPCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 QHKQRRCS--LSSMEMNIVSGQCSNGNMLYI--GFRGLDGVHCTPTTDSGVI-----
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                               DB 18; Length 502;
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           STUDIES
                                                                                                                                 Example; Fig 2A-B; 18pp; English
                                                                                                                                                                                                                                                                  and their histological location
          (SALK ) SALK INST BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                   Conservative
                               Lindstrom JM, Schoepfer
                                                 WPI: 1997-118297/11
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                        502 AA;
                                                               N-PSDB; AAT59196
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AAW12369 standard; Protein; 511 AA.

AAW12369 ID AAW1 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences of chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtains an 18-day chick embryo CDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact abby subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing antibodies to permit affinity purification of subtypes and their histological location.
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/label= Sig_peptide
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ligand binding; ion channel
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N-PSDB; AAT59197.
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                                                    605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
                                                                                    NPAFYRTVYG-------QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
                                                                                                                 -WIRIVFLCWLPWILRMSRPG---RPL
                                                                                                                                                                                                                                   Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                    Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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29..256
Tabel- TMD1
^^te- "transmembrane domain"
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label- TMD2
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/label= TMD3
                                                                                                                                                                                                                                                                                                                                                                                           /label= TMD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-303024/37
N-PSDB; AAV12197.
                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                   SCKY-
                                                                                                                                                                                                     14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9420617-A2
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1994
                                                                                                                                                                                      AAW44153;
                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human neuronal nicotinic acetylcholine receptor (MAChR) subunit. The cells expressing the alpha and/or beta MAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal MAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIPCVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.7%; Score 1159.5; DB 15;
45.1%; Pred. No. 1.4e-97;
tive 82; Mismatches 115; I
Page 80-81; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                               that express a variety of subtypes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1997
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Ashkenazi AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1999;
                                                                                                             29-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                        08-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment,
                                                                                     AAB24088;
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                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or bete subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%; Score 1159.5; DB 45.1%; Pred. No. 1.4e-97, tive 82; Mismatches 11?
                                                                                                                                                                                                                                                                   Disclosure; Page 73-74; 108pp; English.
                                                                                                                                           (SIBI-) SIBIA NEUROSCIENCEȘ
                                                                                              96WO-US09775.
                                                                                                                     95US-0484722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                       Harpold MM;
ligand-gated receptor
                                                                                                                                                                                             WPI; 1997-065463/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         502 AA;
                                                                                                                                                                                                           N-PSDB; AAT48239
                        Homo sapiens
                                                                                              07-JUN-1996;
                                                                                                                      07-JUN-1995;
                                               WO9641876-A1
                                                                                                                                                                       Elliott KJ,
                                                                    27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local S
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Matches
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those characterised by overexpression and/or activation of the amplified antibode characterised by overexpression and/or activation of the amplified antibode characterised by overexpression and/or activation of the amplified antibode characterised by conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, anglogenic and immunologic disorders. Ac58242 to AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC5836 and AAB24089 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO8109, PRO880, PRO880, PRO8810, PRO941, PRO1025, PRO1009, PRO1025, PRO1090, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1281, PRO23, PRO834, PRO8141, PRO1117, PRO1101, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell troatment, diagnosis and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation; tunourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic-disorder; glandular disorder; morrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour; diagnosis; neoplastic disease; neoplastic cell
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450 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO2145 protein sequence SEQ ID NO:77.
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                                                                                                                                                                                                                      AAB24088 standard; Protein; 502
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99US-0143048.
99US-0145698.
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99WO-US12252
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                                                                                                                                                       67
 of
 PRO polynucleotide and protein sequences given in the exemplification the present invention.
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                                                                                                                                                                                                                                                       474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                         297 IYLNLSAK --- VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                 354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                         TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                               534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                                                             ---WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues
                                                                                               91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; darug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSLASVE-----MSAVAPPPASNGNLLY----IGFRGLDGVHCVP-TP-
                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108..115 /note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trp108 and Tyr115 are essential
                                                                    21;
                                                                    DB
                                                                   Score 1159.5; DB
Pred. No. 1.4e-97
2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotinic acetylcholine receptor alpha7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB82690 standard; Protein; 502
                                                                                             82;
                                                                               45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2001 (first entry)
                                                                               al Similarity 45.1
237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171..173
                                         502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82690;
                                                                                                                                                                                                                                       114
                                         Sequence
                                                                   Query Match
Best Local
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                                                                                             Matches
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12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Water-soluble ligand-binding proteins derived from molluscs and analogues of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 KNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||:| ::| | |:||||||||:| ||: |||| | ||:|||||:| ||:||||:|:
TNVLNNSSGHCQYLPPGIFKSSCXIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AChBFS) and analogues of ligand-gated ion channels, their crystals, and their use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming multimers and are amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels. Chimeric proteins are provided that are capable of con channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-ested receptor, and comprise at least the amino acids of the AChBP determining solubility of the conservations of the esseme positions as in the AChBP, and also comprising amino acids determining binding to the ligand. In the chimeric proteins are substituted for the conservation of the essential amino acids of the essential amino acids of the essential amino acids of the conservation of the essential acids of the conservation of the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 GDISSYVLNGEWELLGVPCKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is.
"conserved ligand-binding region, residues Tyr210, Cys212, Cys213 and Tyr217 are essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding amino acids, and preferably entire stretches have
been substituted. New drugs can be developed that selectively
intervene in neuronal signalling pathways, especially where the
ligand-gated ion channel is the nAChR, and the related disorder
Tourette's syndrome, Alzheimer's disease, addiction to nicotine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%; Score 1159.5; DB 45.1%; Pred. No. 1.4e-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 252-254; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                  (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                                                                                                                                                                                                                  2000EP-0200443.
2000EP-0203810.
                                                                                                                                                                                                                 09-FEB-2001; 2001WO-EP01457
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Best Local Similarity 45.15
Matches 237; Conservative
        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                       Sixma TK;
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                                                                                                           WO200158951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizophrenia
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31-OCT-2000;
                                                                                                                                                            16-AUG-2001
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        ###X4X4X4X4X4X
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413 127 473 184 533 244 581

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------DSGVV----CGRMACSPTHDEHLLHGQPPEGDPDLAKILEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                                                                                             NAChR; drug screening;
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TWULNUSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 GLSVVVTVIVLQYHHDDPDGGKMPKWTRVILLINWCAWFLRMKRPGEDKVRP-ACQHKQRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                           INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                         IYLNLSAK - - - VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                          KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                  GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                      ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell comprising nucleic acids encoding human alpha and beta subunits neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Siegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nicotinic acetylcholine receptor; NAChR alpha7 subunit; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chavez-Noriega LE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neuronal NAChR alpha7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB82435 standard; Protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001WO-US50985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC
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N-PSDB; ABV73248.
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                      297
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ABB82435
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                                                                                                                               612
  ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI 244
                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Нď
                                                               SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                                                                               ---WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                        305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR
                                                                                                                                                                                                                CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                                              669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                                                                                                                                                                                    -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1.4e-97;
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                                           ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                             DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                 28.7%; Score 1159.5; DB 22; Lengt
45.1%; Pred. No. 1.4e-97;
.ive 82; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type human alpha7 ligand gated ion channel
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N-PSDB; AAC90380.
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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicothinic acetylcholine receptor (NACHR). The compositions and methods of the present invention, which provide a means to prepare systhetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NACHR alpha? subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
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                                                                                                                                                                                                                                                                                                               -97;
115; Indels
                                                                                                                                                                                                                                                                                        DB 23;
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ion flux; alpha
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US6440681-B1

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
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                                                                                                                                                                                                                                          Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to nNACAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1159.5; DB 23;
Pred. No. 1.4e-97;
                                                                                                                                                                                                                                                                                                                 Claim 101; Column 59-64; 56pp; English.
                                                                                                                                                                       Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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45.18;
                                                                  90US-0504455.
92US-0938154.
93US-0028031.
                                       95US-0487596
                                                                                                             93US-0149503
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Best Local Similarity 45.1
Matches 237; Conservative
                                                                                                                                          & CO INC
                                                                                                                                                                     Ellis SB,
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                                       1,5661-NUC-70
                                                                                                             08-NOV-1993;
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                                                                                                                                                                     Elliott KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAchR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAchR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha? NAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                                                                                        Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 IYLNLSAK --- VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding variant of human alpha? nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the exceptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
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DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                ODESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGTIGMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monteggia LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 1155.5; DB 45.0%; Pred. No. 3.4e-97 iive 82; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McKenna DG,
                                                                                                                                                                                                         V274T variant human alpha7 nAChR protein.
                                                                                                            AAW69216 standard; Protein; 502 AA
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Sullivan JP, Touma
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SALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
                                                                                                                              184
                                                                           TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
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Perfect score:

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BG632919 885 bp mRNA linear EST 23-APR-2001 GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila;
I (bases 1 to 885);
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
Unpublished
Other_ESTS: GH16126.5prime
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
sax: 510 48/6 fvy.
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
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ALO73676 Drosophil
ALO64281 Drosophil
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

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BX299163 BX299163

ACC53497 MUS TRUSCU AKC651730 MUS TRUSCU AKC081224 MUS TRUSCU AKC081224 MUS TRUSCU AKC081224 MUS TRUSCU BK639934 170006876 BU149265 AGENCOURT BU516733 BB160023A AKC080475 MUS TRUSCU BU516843 BB160023A AKC080475 MUS TRUSCU BU711715 UT-E-CL1 AW911206 EST345510 BW711715 UT-E-CL1 AW914206 EST345510 BW73108 MUS TRUSCU CA373068 MUS TRUSCU CA373068 WUS TRUSCU CA373068 WUS TRUSCU ALT10017 GH09582.5 BU195149 GC0244157 AKC30464 MUS TRUSCU CA374163 648474 NC BU919212 GC01-01 M BG404575 GO242021

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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic ABO03511: arm:X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
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/mol_type="mRNA"
/db_xref="taxon:7227"
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6e-92;
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Pred. No. 6e-92,
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/dev_stage="adult"
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Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifify.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                       DNA linear GSS 03-JUN-1999 survey sequence T7 end of BAC #
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                    DNA linear GSS 03-JUN-19
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR02C08 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 1.8e-69;
L; Mismatches 4
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/note="end : T7"
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llarity 98.5%;
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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                                                                                                                                                                             Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK13K13 Lof RPCI-98 library from Drosophila melanogaster (fruit AL064281 Gruvey sequence.
AL064281 GI:4944356
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Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage BP 191 91006 EVRY cedex · FRANCE (E-mail : seqrefégenoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Mooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 1.9e-67;
0; Mismatches 2; Indels
                             1353 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCT 1391
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/db_xref="taxon:7227"
/clone="BACR13K21"
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Web: www.genoscope.cns.fr.

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                                                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACK35F05 of RPCI-98 library from Drosophila melanogaster (fruit AL0/73676
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1; Mismatches 5;
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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GH15518.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH15518 5 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. AI292581
AI292581.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. [ toases I to 607) Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
                                                                                                ACAGTGCGGATGAGGGATTTGACGGCACCTACCAGACGAACGTGGTGGTGCGGAACAACG
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                                                                                                                                                                                                                                                                        1385 TCCAGCTGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCA
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003626: arm:2L [9617316,9882551]
estlmated-cyto:30C7-30F4: 04/10/2001
plate: GH.155 row: B column: 6
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Drosophila melanogaster
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Contact: Stapleton, M.
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// Organism="Homo sapiens"
// Organism="mankA"
// Organism="mankA"
// Organism="Lare" | Organism="manka" |
// Organism="manka" |
// Organism="manka" | Organism="manka" |
// Organism="manka" | Organism="manka" |
// Organism="manka" | Organism="manka" |
// Or
                                                                                                                                                                                                                                                                                                          1201 bp mRNA linear EST 23-MAY-2003 AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CSODD007xP05 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCTGCACGTGTCCCTGCAAGCGAGTWCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGA 229
   CTGCTAAAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03QP1&cluster=7646.r. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTATAATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTG
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Pred. No. 3e-57;
5; Mismatches 322; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Feb 13, 2001 this sequence version replaced gi:12793792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini; Hominidae; Homo.
                                                                                                                                     GATGAAGTTCGGCAGTTGGACCTACGACGATTCCAGGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                   1353 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL530299.2 GI:31068132
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Best Local Similarity 59.8%;
Matches 503; Conservative
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1682

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can be

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/mol_type="mRNA"
/db_xref="taxon:8355"
/dclone="thAGE:6642638"
/tissue_type="cocytes"
/lab_host="bH10B (phage-resistant)"
/clone_lib="NICHD_XGC_OOI"
/note="vector: pCWV-SPORTS, Site_l: Not!; Site_2: Sall;
/note="vector: pCMV-SPORTS, Site_1: Not!" Site_2: Sall;
/note="vector: pCMV-SPORTS, Site_1: Not!; Site_2: Sall;
/note="vector: pCMV-SPORTS, Site_2: Sall; S
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051 GTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111 ATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 TACTATTTGCAGTGGAACATGTCTGAATACCCTGGGGTAAAAATGTTCGTTTTCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 CATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATTTGACGGC
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                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
Plate: LLAM14228 row: f column: 14
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Pred. No. 5.7e-46;
0; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 746.
Location/Qualifiers
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60.0%;
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                                                          Tumor Gene Index
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Best Local Similarity
Matches 415; Conserv
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     AUTHORS
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                                                                                                                                                                                                               /sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head poT2"
/note="Organ: head; Vector: poT2; Site_1: EcoR1; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  896
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Mombibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
1 (bases 1 to 922)
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IMAGE:6642638 5', mRNA sequence.
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                                                                                                     /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db xref="taxon:727"
/clone="GH15518"
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Pred. No. 3.1e-53;
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Xenopus laevis
High quality sequence stop: 521 POLYA=No.
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 60000 Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                        1651 TTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCGAG 1710
                                                                                                                                                                                                                                                                                                                      HTC 05-DEC-2002
                                                    628 ATCTCACTTGGTATAACAGTCCTATTGTCCCTCACTGTGTTCATGCTGTTGGTAGCTGG 687
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                              1711 ACAATGCCGGCTACTTCCGATGCGGTGCCATT 1742
                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
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/tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTTNVWVKQEWHDYKLRW
DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFYDGRVQWTPPAIYK
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHH
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLMMFIIVCLLGTVGLFLPPW
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                                                                                                                                                                                        Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIRRD), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                         Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kotawa, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sayao, H., Sayai, C., Sakai, K., Sakazume, N., Sayao, H., Sayai, M., Sayai, T., Tanaka, T., Toya, T., Yasunishi, A.,
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
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/note="unnamed protein product; cholinergic receptor,
nicotinic, alpha polypeptide 4 (MCD|MGI:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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Pred. No. 3.2e-45;
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/db_xref="taxon:10090"
/clone="9330165116"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="G1:26329799"
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                                                              of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2940)
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/strain="C57BL/6J"
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                                                                                                      989 ITCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAATTATCG 1048
                                                                                                                                                                             ATGIGGACGAGAAAAATCAATIGCTÄGICACIAAIGIGIGGITAAAACIGGAGIGGAACC 1108
                                                                                                                                                                                                                                                   ACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGC 1168
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AR083157
                                                                                                                            525 TCACCCACCTAACCAAAGCCCACCTGTTCTATGATGGGCGTGTGCAGTGGACACCCCCGG
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                                 929 ATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACGTCCCG
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UI-M-FYO-cds-b-06-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone IMAGE: 6833671 5', mRNA sequence.
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This clone was contributed by the Brain Molecular Anatomy Project
445 TCACCCACCTAACCAAAGCCCACCTGTTCTATGATGGGCGTGTGCAGTGGACACCCCCGG 504
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
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                                                  1289 GGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAGCGGT
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_nost="DH108 (TI phage resistant)"
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/strain="C57BL/6"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
36 .1925
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RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTINVWVKQEWHDYKLRW
DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFYDGRVQWTPPAIYK
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
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EPGILGDICNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWWFIIVCLLGTVGLFLPPW
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  RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 TAGCCAATATCTCAGATGTGGTCCTTGTCCGCTTTGGCTTGTCGATTGCTCAGTTG
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                     Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp./
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/db_xref="taxon:10090"
/clone="C630019M18"
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                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="GI:26350297"
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          // Actobe="Organ into_Enrary."
// Actobe="Organ into_Enrary."
// Actobe="Organ into_Enrary."
// Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dry
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGACACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator.

71 a 257 c 199 g 203 t 3 others
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/clone_lib="NIH_BMAP_FY0"
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/organism="Mus musculus"
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/tissue_type="mhole brain"
/tissue_type="mhole brain"
/tissue_type="mhole brain"
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/lab_host="NH_BHAP_FID"
/clone_lib="NH_BHAP_FID"
/clone_lib="NH_BHAP_F
                                                                                                                                                                                           A linear EST 09-OCT-2002
Mus musculus CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs remail.nib.gov
Tissue Procurement: Dr. Jim Lih., University of Iowa
Tissue Procurement: Dr. Jim Lih., University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed Dy: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINIA at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAA
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.3e-42;
0; Mismatches 299; Indels
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UI-M-FIO-byx-p-12-0-UI.rl NIH_BMAP_FIO MMAGE: 6400763 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Robert Strausberg, Ph.D.
ATCNACGAGATCATCNCGTCCACCTC 743
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225 c 188 g
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Location/Qualifiers
1. 755
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S., Aizawa, M., Nishi, K., Kiyoswa, H., Kondo, S., Yamanaka, I., Saito, T., Gajobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasaterland, T., Gissi, C., King, B., Kochlwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washlo, T., Sakai, K., Okido, T., Fuunco, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Boffelli, D., Bolinga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, M. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Williang, L., Toyo-oka, K., Wang, K.H., Weltz, C., Wiltaker, C., Williang, L., Mynshaw, Bolis, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIRBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/strain="G57BL/G3"
/db_xref="FANTOM_DB:4831406G09"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
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                                                                                                                    ATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGA 1221
                                                                                                                                                                                                                                                           TTTGACGGCÁCCTACCAGACGAACGTGGTGGTGCGGAACAACGGCTCGTGTCTATACGTT 1281
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       CCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGAC
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/cell_line="CK-KI"
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/cloe_lib="Li5cKKI"
/cloe_lib="Li5cKKI"
/rote="Organ: Liver; Vector: pCNS-D2; Site_l: EcoRI;
Site_2: NotI; The poly (A+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                                                                                                                                                                                                                                             CB149460 615 bp mRNA linear EST 29-JAN-2003 K-EST0205995 L15CKK1 Homo sapiens cDNA clone L15CKK1-50-D08 5',
                                                                                                                                                                     1624 ACCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTG 1683
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Buwaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 615)
1 (bases 1 to 615)
1 (homo. Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R. R.Y., Chong, J.E., Sohn, H.Y., Kim, J.W., Park, H.S., Kim, S. and Kim, Y.S.
1684 ACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG
                                                                                                                                                                                                                                                                                                 1564 TATTTCTTCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTC
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Email: 90ngsung@mail.kribb.re.kr
Plate: 50 row: D column: 08
High quality sequence stop: 615.
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Unpublished
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/db_xref="taxon:9606"
/clone="L15CKK1-50-D08"
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HREIVQVTVGLQLIQLINVDEVNQIVTTNVRLKQQWVDYNLKWNPDDYGGVKKIHIPS
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                                                 /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                         /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
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nes 388;
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Pred. No. 6.26
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                                                                        /dev_stage="0 day neonate
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/protein_id="BAC26337.1"
/db_xref="G1:26325166"
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Mus musculus 0 day neonate eyeball CDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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                                              1203 CAACAGTGCGGATGAGGGATTTGACGGCACCTACCAGACGAGGAGGTGGTGGTGCGGAACAA 1262
                                                                                                          1263 CGGCTCGTGTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCAC 1322
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                                                                                                                                                                                                                                                                                                                                  291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                              181 CTGGTCCTTGGATCTGCAGATGCAGGAGGCA-----GATATCAGTGGCTATATCCC
                                                                                                                                                                                                                                                                                                                     CGATATTGCTGATAAACGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTC
                                                                                                                                                                            GTGGTTCCCCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGG
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              Indels
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
 No. 1.3e-41;
Pred No. 1.3e
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Mus musculus
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 64.18;
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Kawai,J., Shinaqawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Arakawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Osazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casayant,T.,
Fleischmann,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuchl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K., Hasesgawa,Y., Kawaji,H., Kohtsuki,S.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lof 60,770 full-length cDNAs

E (bases I to 1864)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Rukuda,S., Furuno,M., Hanagaki,T., Haranco,K., Hiramco,K., Haraka,T., Hrozane,T., Hayashida,K., Ishii,Y., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakaura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,D., Saitoh,H., Sakai,C., Sakai,K., Sakai,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

AL Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, Rax:81-45-503-9212, Pexx:81-45-503-9216)
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wathhiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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Encyclopedia Project of Genome Exploration Research Group in R
Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
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AK051730.1 GI:26342155
HTC; CAP trapper.
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/db_xref="FANTOM_DB:E130103E14"
/db_xref="taxon:10090"
/clone="E130103E14"
/tissue_type="syeball"
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/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                  /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 TAACGTGTCCCATCCTGTCATCATCCAGTTTGAGGTGTCTATGTCTCAGCTGGTGAAGGT
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AK051730 2916 bp mRNA linear HTC 05-DEC-2002 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN FUILl-length enriched library, clone:0130068406 product:WEDNGNAL NICCTINIC. ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
         CGCCATCATCATCCGCCGACGAACACTGTACTATTTCTTCAACCTGATCATACCTTGTGT
                                                           1593 ACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGTGAAAATT
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L. Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
                  Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringyae, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weltz, C.C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_atge="12 days embryo"
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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
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LIVPELVITETIPSTSLYPILGEYLLETMIRYTLSIYITYSYLNHYRPTTHTMPT
WKRAPFINLLPRVMEMTRFTSFEDAPKTHSYGAELSINLNCFSRADSKSCKEGYPCO
DGTCGYCHHRRVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIABENK
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                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2916)
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                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.
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URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
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Drosophila melanog Drosophila melanog

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	Acetyl-choline receptor neurotransmission; plan Drosophila melanogaster	٠ بـ ٠	nicot prote	nicotinic; insect; insecticide; protection agent; conductance;	de; screening; e; AChR; ds.
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                                                                                                   This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (III). This sequence encodes an acetyl-choline
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                                                 encoding a nicotinic acetylcholine receptor identify potential insecticides
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      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176 ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                        CACAGCAACATTGCAAGCGAGCAGCAATAGCCAGCAACAGGAGCCAGCATCGAAGGAC
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Qy 838 AGCACGCAAATATTAAACGGACTTAATAAACACTCATGGATATTTTTATTGATATTTG 897	Db 1121 AACAAGGGCACAACCAGCAACTCACAACACTGCAACCAAGGAGCTTAAGTACAAAACAC 1180
Db 841 AGCACGCAAATATTAAACGGACTTAATAAACACTCATGGATATTTTATTGATATTTTG 900	Qy 181 CACAGCAACATTGCAAGCGAGCAGCACAATAGCCAGCAACAGGAGCCAGCATCGAAGGAC 240
Qy 898 AATTTATCTGCTAAAGTTTGC 918	Db 1181 CACAGCAACATTGCAAGCGAGCAGCAACAATAGCCAGCAACAAGGAGCCAGCATCGAAGGAC 1240
Db 901 AATTTATCTGCTAAAGCAAGC 921	241 GAGGATGTAGCCAACCGCTAGAAGCAATGACCAGCAGCGACTGTGCAACACGCTAGAC
RESULT 3	1241 GAGGATGTAGCCAACCACGGTAGAAGCAATGACCAGCAGCAGCACCATCTGCAACACCTAGAC
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XX AC ABL27130;	1501 AGGGGAACATGTTGTCGCCAAAAAACAGGCAGCAGCAACTGCTGCCGGGGAGAACAGAACAAACA
XX T 26-MAR-2002 (first entry)	
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863.	
XX M. Drosophila; developmental biology; cell signalling; insecticide; KW pharmaceutical; gene; ds.	CONCORDADA MANAGERA CONCORDA CONTROLLA MANAGERA
XX OS Drosophila melanogaster.	Оу 464 463
XX PN WO200171042-A2.	Db 1481 ATCATATTTAACTAAATATATAGAAATTTAGAAAATAATTGCACCCTCAGCACTTGAATT 1540
XX PD 27-SEP-2001.	Qy 464AGAAACAACAGCAACTTAGCATGCCTCCCTTCAAAACGCA 505
XX PF 23-MAR-2001; 2001WO-US09231.	Db 1541 TGGTCTTCTTACAATTGCAGAAACAACAACGAACTTAGCATGCCTCCTTCAAAAACGCGCA 1600
XX PR 23-MAR-2000; 2000US-191637P. PR 11-JUL-2000; 2000US-0614150.	506 AATCCACGGACACCTACAGCACCAGCAGCAACAACCAGCTGTCCGACAGCTACTACA
XX PA (PEKE ) PE CORP NY.	1601 AATCCACGGACACCTACAGCACACCAGCAGCAATAACCAGCTGTCCGACAGCCACCTACA
XX PI Venter JC, Adams M, Li PWD, Myers EW;	566 TGCAATGTCGAGCCAGCGACAATGAGTTCAGTATTCCGATATCGAGACATGATAAGTAT
WPI; 2001-656860/75.	1661 TGCAATGTCGAGCCAGCGACAATGAGTTCAGTATTCCGATATCGAGACATGATAGATA
New isolated nucleic acid detection reagent for detecting 1000	
genes from Drosophila and for elucidating cell signalling and ce interactions -	1/21 CCACGGCCACATTCGCCTGTGTGCCTGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
XX PS Claim 1; SEQ ID NO 32863; 21pp + Sequence Listing; English. XX	Oy 686 AGTGGCAACTTCACGTGCAACGCGATCGGTGCTACTGTTCAAAAGGATCGCAACAA 450
	746 CCATCGCTTCATTTCATTTTAGGCAGCTTTGCAGCGCAACTGAAAATAGCAGCCA
useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of	1841 CCATCGCCTTCATTTCCTATTTAGGCAGCTTTGCAGCGCAACTGAGGAGCAGCAGCAGCAGATA
	QY 803 GCAGCAGTAGCAGCAGCAACAACAACAACAACAGCAGCACGCAAATATTAAACGGACTTA 862
	DD 1901 GCAGCAGCAACAGCAGCAACAGCAGCAGCAGCAGCAGCAG
CC The sequence data for this patent did not form part of the printed . CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.	863 ATAAACACTCATGGATATTTTATTGATATTTGAATTTATCTGCTAAAGTT 915
XX SQ Sequence 3144 BP; 1056 A; 676 C; 680 G; 732 T; 0 other;	DD 1901 AFAAACACTCAFGGAFATTTTAFTGAFAFTFGAATTFATCTGCFAAAGG 2013
ore 776.2; DB 23; Length 3144; ed. No. 5.5e-206; Wigmathhod 13; Indole 08.	RESULT 4 ABL07799 TD ABL07790 standard. CDNA. R03 RD
Marcnes 902; Conservative U; Mismarcnes 13; indeis 96; Gaps	ABLO(199 Staintain; CDNA; 603
Oy         1 ATGARANATGGAAATGAAGTGAGTGAGAGATGAGCAGTGTGGCAGTGTGAGAT           1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AC ABLO(799; XX XX DT 26-MAR-2002 (first entry)
Qy 61 AGATTAGCGCACTGCAGCAGCAGCACTTTAGCAGCAGAGCACAAGAACCACCAGCAGC 120	XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17879.
Db 1061 AGATTAGCGCACTGCAGCAGCAGCAGCAGTAGCAGCACAAGAACCACCAGCAGC 1120	XX X Drosophila; developmental biology; cell signalling; insecticide; KW pharmaceutical; gene; ss.

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TCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCGAGACA 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agenits that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (1) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Hellothus virescens.
                                                            GCCATCATCATCATCGCCGCGACGAACACTGTACTTTCTTCAACCTGATCATACTTGTGTA
                                                                                                                        CTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGTGAAAAATTA
                                                                                                                                             GCCATCATCATCGCCGCGGACGACACTGTACTATTTCTTCAACCTGATCATACCTTGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention issell in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7777-ABB72072).

The sequence adta for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 88.45
Matches 616; Conservative
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11-JUL-2000;
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                                      GGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACGT
                    Gaps
Length 3700;
                   Indels
DB 21;
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Score 512.8;
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2166 2286 18 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins or more CCACACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGCATTGGG CTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCAATGCTGCCGATAC 2047 CCAATTGGCAGCACCCGAATGCCGGATGCGGTCACCATCATACGTGCATCAAATCATCA AAGGACGACGAAGATGCGGACATTTCGCGCGACTGGAAGTTCGCCGCCATGGTCGTGGAC AGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCACAATAGCTGTACTACTA AAAGAIGACGAGIGCAAIGACATIGCCAAIGAIIGGAAAIITIGCAGCIAIGGICGIIGAC 2107 ACTGAATATGAATTAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAGCTACGT NO 35681 developmental biology; cell signalling; insecticide; detection reagent for detecting 1000 for elucidating cell signalling and ID NO 35681; 21pp + Sequence Listing; English. G

(first entry)

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                            214 CTCATGCAGATTATCGATGTGGACGAAAGAATCAACTGCTTATAACGAATATTTGGCTC
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                                 Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;
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Pred. No. 3.5e-123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175
                                                    developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                        1565 ATTTCTTCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCA 1624
                                                                                                                                                                                                          CCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGA 1684
                                                                                                                                                882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant
                                           CCCCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCA
                                                                    GCTGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGG
                                                                              CGAGTGGGAACTACTGGGT----GTGCCCGGCAAACGTAACGAGATCTATACAACTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding a nicotinic acetylcholine receptor from ed to identify potential insecticides \,
                                                                                                                                                                                                                                                                                                                                                                          nicotinic; insect; insecticide; scree protection agent; conductance; AChR;
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P-PSDB; AAY50816.
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protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                                                                                                                                          AGGICCTCACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCG
                                                                                                                                                                                                                                                                                                                                                                   TCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                           1044 TATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAAT
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                                                                                                                                                   Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  971
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                                                                                                                                                                                              DB 21;
                                                                                                                                                                           Score 411.4; DB 41;
Pred. No. 5.3e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGACAT
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                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 17876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14668;
                                                                                    developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                               (first entry)
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                                                                                                   pharmaceutical; gene; ss
                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                   /enter JC, Adams M,
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P-PSDB; ABB63695
                                                                                                                                                          WO200171042-A2
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO31, PRO1005, PRO1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy
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1300 GATGAAGTTCGGCAGTTGGACCTACGACGATTCCAGGT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO2145 nucleotide sequence SEQ ID NO:76.
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                                                                                                                                                                                                                                                                               AAC58395 standard; cDNA; 1509 BP
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99WO-US30911.
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coding sequence

ion channel

(first entry)

channel;

2000WO-US11862

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Human; alpha7 nicotinic acetylcholine gated ion chann
5-hydroxytryptamine; 5-HT3; calcium ion conductance;
                                             Wild-type human alpha7 ligand gated
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                                                                                                                                                                                                                                                                                                               971 ATACACTAGAAGGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAA 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent hum
PRO polynuclectide and protein sequences given in the exemplification
the present invention.
                                                                                                                                                                                                                             AAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATA
                                                                                                                                                                                                                                                           ACGIGICCCIGCAAGGCGAGITCCAGAGGAAGCITTACAAGGAGCTGGTCAAGAACTACA
                                                                                                                                                                                                                                                                                                                                          TAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTA
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                                                                                            Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                                                                                                                  Mismatches 318;
                                                                                                                                     Score 296.2; DB : Pred. No. 5.8e-72
                                                                                                                                                                                  ٠<u>;</u>
                                                                                                                                     12.8%;
60.7%;
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                                                                                                                                                                                                                                                                             The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chima7/5-HT3 chimeric ligand gated ion channel (see AAC903932 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 AAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296.2; DB 22;
Pred. No. 5.8e-72;
0; Mismatches 318;
                                                                                                                                                                                                                                   5; Pages 60-61; 77pp; English
  Berkenpas MB;
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nilarity 60.7%;
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standard; cDNA; 1509

AAC90380

RESULT 11 AAC90380 AAC90380

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                                                                                                                             AGTGGGAACTACTGGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGG
                                                                                                                                                                                             CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT
                                                                                                                                                                                                         CTGCAGATTCCGGGGAGAAGATTTCCCTGGGGATAACAGTCTTACTCTCTTTACCGTCT
                   CCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGGAGGCTGGTCCT
                                     TGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG
                                                                                               AATGGGACCTAGTGGGAATCCCCGGCAAGAGGAGTGAAAGGTTCTATGAGTGCTGCAAAG
                                                                                                                  AACCCTATATAGACATCACCTTCGCCATCATCGCCGCCGACGAACACTGTACTATTTCT
                                                                                                                                                       TCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "neuronal nicotinic acetylcholine receptor alpha-7 subunit"
                                                                                                                                                                                                                                    TTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
                                                                                                                                                                                                                                                                                                                                                                                    Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                TCATGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATTG
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             Nach Subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
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receptor (NAChR) subunit. The cells expressing the alpha and/or beta
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                                                                                                                                                                                                                                                                                                                   that express a variety of subtypes
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AGGATCTGCGAATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTG 1210
                                                          CGGATGAGGGATTTGACGGCACCTACCAGACGAGCGTGGTGGTGCGGAACAACGGCTCGT 1270
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                                                                                                                                                                                                                                                    TGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG 1450
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immunochemistry; NAChR alpha7 subunit; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elliott KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1691 TTCTGAATATGCTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
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  "neuronal nicotinic acetylcholine receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neuronal NAChR alpha7 subunit encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 73..1581
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                                                                                                                                                                                                                            neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that
                 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
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Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296.2; DB 18; Length
Pred. No. 6.5e-72;
); Mismatches 318; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
                                                                                                                                                                                                                       Neuronal nicotinic acetylcholine receptor; nAChR;
ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 71-73; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulate the activity of human nAChRs
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
73..1581
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tes 506; Conservative
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                                                                                                AAT48239 standard;
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                                                                                                                                                                                                isolated nucleic acid molecule comprising a sequence of nucleotides or inhomolecules that encodes at least one alpha or beta subunit of a human neuronal nicotinic acctylcholine receptor (NaChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
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                                                                   Cell comprising nucleic acids encoding human alpha and beta subunits neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                    invention relates to a suitable host cell transfected with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 296.2; DB 24; Length 1876;
Pred. No. 6.5e-72;
0; Mismatches 318; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
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                                                                                      895
                  CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT
                                                                                      836 CTGCAGATTCCGGGGAGAAGATTTCCCTGGGGATAACAGTCTTACTCTCTTACCGTCT
                                                                                                                                                                                                                                                                                                                   Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA
                                                                                                                      TTCTGAATATGCTGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
                                                                                                                                  TCATCTCCTCCTCGTCGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATTC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NNACHR.
                                                                                                                                                                                                                                                                                                                                               n; neuronal nicotinic acetylcholine receptor; nNAChR; gene; flux; alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying antagonists or agonists of human neuronal nicotinic
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Search completed: August 21, 2003, 04:24:33 Job time : 625.968 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nuc	OM nucleic - nucleic search, using sw model	
Run on:	August 21, 2003, 00:04:15; search time 8610.32 Seconds (without alignments) 10975.350 Million cell updates/sec	32 Seconds s) cell updates/sec
Title: Perfect score: Sequence:	US-09-303-232-1_COPY_372_2681 2310 1 atgaaaaatgcacaactgaacaccacatattattgtctcg 2310	tgtctcg 2310
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2888711 seqs, 20454813386 residues	
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Database :	GenEmbl:*  1: gb_ba:* 2: gb_htg:* 4: gb_in:* 5: gb_ov:* 6: gb_pat:* 6: gb_pat:* 8: gb_pl:* 8: gb_pl:* 10: gb_ro:*	

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DEFINITION Sequence I From Facenc EP0902320.	N AX009610	AX009610.1 GI:9996842		Drosophila melanogaster (fruit fly)	SM Drosophila melanogaster	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Ephydroidea; Drosophilidae; Drosophila.		S Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.	Nucleic acids encoding acetylcholin-receptor subunits from insects
DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		e.		REFERENCE	AUTHORS	TITLE

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em\_htgo\_mus:\* em\_htgo\_other:\*

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PIGSTREMDANYHHTCIRSSTPSELGLILKEIRFITDQLRKDDECNDIANDWRFAAMV
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/mol type="qenomic DNA"
/db_xref="taxon:7227"
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/note="unnamed protein product"
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                                                                                       Length, 2886;
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/organism="Drosophila melanogaster"
/mol.type="qenomic DNA"
/db_xref="taxon:7227"
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                                                         TTGTGGATACGCATCGTGTTTTTGTGCTGCTGCCATGGATATTGCGAATGAGTCGCCCA
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   JP 2000023680-A/I.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroida; Drosophilidae; Drosophila.
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Nucleic acid encoding insect actyl choline receptor subunit
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VOVLLVYLOOWGLHYOORSVLLFRILAASTTAFISTIGSFAQLKRSSSSSSSNSS
NNS STOILNGLNKHSWIFLLIYINLSAKVCLAGYHERRLLHDLLDPYNTLERPVLNES
PLOLSFGLTLAGINKHSWIFLLIYINLSAKVCLAGYHERRLLHDLLDPYNTLERPVLNES
PLOLSFGLTLAGINDDELVOLYNWAKLEWNDNNLRWTSDYGGVKDLRIPPHR
EWRFGSWTYDFQLDLOLDODTGGDISSYVLNGEWELLGYPGKNDITYYNCCPEPYID
ITFAIIIRRRILYYFERNLIYFOYLIASMALLGFTLPPDSGRKLSLGYTILLSLTYFUN
WVAETMPATSGAVPLLGTYFRUINRWYSSSYVSTILILNYHHRNADTHEMSEWIRIYF
LCMPWILIRARSRRGTLYTEPTTPGSTSSERSKELSKSTLAVVLDI
DDDFRHNCRPWTPGGTLPHDAFYRYYGGGDDGSIGPIGSTRMPDAYTHTGISSY
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/note="results in asparagine
compared to B allele"
/replace="g" 634 t
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//gene="nAcRalpha-34E"
//note="results in deletion of
compared to B allele"
                                                                                                                                                                                                                                                                   /gene="nAcRalpha-345"
/note="results in threonine
compared to B allele"
/replace="t"
1079. .1080
                                                                                                                                                           /gene="nAcRalpha-34E"
/note="compared to B allele"
/replace="a"
375
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/gene="nAcRalpha-34E"
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compared to B allele"
/replace="gg"
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Pred. No. 0;
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insertion; compared to B a
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llarity 95.4%;
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INV 30-APR-2002
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//gene-inAcRalpha34E"
//note="ion channel; neurotransmitter transmembrane
receptor; exon 5 is excluded due to exon skipping, which
generates a loss of reading frame and a truncated
polypeptide; alternatively spliced"
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2834 bp mRNA linear INV 30-APR-200 melanogaster nicotinic acetylcholine receptor Dalpha5 nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
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                                                                                                                                                                                                                                                                                                         la melanogaster (fruit fly)
la melanogaster
s, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
: Endopterygota; Diptera; Brachycera; Muscomorpha;
ea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (25-MAY-2001) MRC-FGU Human Anatomy and Genetics, y of Oxford, South Parks Road, Oxford OX1 3QX, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%; Score 1994.8; DB 3; Length 2834; 91.7%; Pred. No. 0;
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/mol_type="mRNA"
/db_xref="taxon:7227"
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    .2834
    /gene="nAckalpha34E"
    /allele="B"
    .1737

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="2"
/map="34E4-34E5"
                                                                                                                                                                                                                                      1 GI:20340268
                                                                                                                                               vely spliced.
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	Qy Dp	Å da ₹	ନ ପ୍ର	Qy	Qy Db	Qy	Qy	Qy	. YO	QY	RESULT 6 AC092243/c	ACCESSION VERSION	AEIWOKUS SOURCE ORGANI	REFERENCE AUTHORS				TITLE JOURNAL REFERENCE AUTHORS
2493 AAAGATGAGAGTGCAATGACATGATGATTGGAAATTTTGCAAGCTATGGTAAGATTTTGAAATTTTTGAAGATGATTGAT	7 AGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCACAATAGCTGTACTA	2287 TCGGCACCACATATTGTCTCG 2310 	RESULT 5	AC017620 ION Drosophila n ON AC017620	VERSION ACUITOLU I GI:553437/ KEYWORDS HTG: HTG: HTG: PHASE2. SOURCE Drosophila melanogaster (fruit fly) ORGANISM Drosophila melanogaster	Euraryota; Medazoa; Artinopoda; Hezapoda; Insecta; Prerygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	AL.			/mol_type="genomic DNA" /db_xref="taxon:7227" /db_xref="taxon:7227" ORIGIN	Ouery Match 33.6%; Score 776.2; DB 2; Length 42079; Best Local Similarity 89.0%; Pred. No. 2.5e-201; Matches 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2;	1 ATGAAAAATGCACAAACTGAAACTGAAGTTGACGATGATGATGAGGGCTGGCT	61 AGATTAGCGCACTGCAGCAACTTTAGCAGCAGTAGCAGCACAAGAACCACCAGCAGC 120 	121 AACCAGAGGCACAACCAGCAACTCACAACACAGGAGCTTAAGTACAAAACAC 180 	181 CACAGCAACATTGCAAGGGGGGGCACAATAGCCAGCAACAGGGGGCCAGCATCGAAGGAC 240 	241 GAGGATGTAGCCAACCACGGTAGAAGCAATGACCAGCAGAGAGCATCTGCAACAGCTAGAC 300 	301 ACCAGCAACATGTTGTCGCCAAAGACCGCAGCAGCAACTGCTGCTGCCGCGATGAAGCA 360 	361 ACAACCCAACAACAACAAAACATAAGACTGTGTGCACGCAAGCGACGACGATTGCGTCGC 420 

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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Erkaryota; Netazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bropteryota; Diptera; Brachycera; Muscomorpha;

Enkaryota; Drosophilae;

Enkaryota; Drosophilae;

Enkaryota; Drosophilae;

Drosophilae;

I (bases 1 to 272521)

Adams, M. D., Celniker, S. E., tholt, R. A., Evans, C. A., Gocayne, J. D.,

Ananatides, P. G., Scherer, S. E., Li, P. W., Hoskins, R. A., Galle, R. F.,

George, R. A., Lewis, S. E., Richards, S., Ashburner, M., Henderson, S. N.,

Sutton, G. G., Wortman, J. R., Yandell, M. D., Zhang, Q., Chen, L. X.,

Brandon, R. C., Rogers, Y. H., Blazej, R. G., Champe, M., Pfelifer, B. D.,

Wan, K. H., Doyle, C., Baxter, E. G., Helt, G., Nelson, C. R., Gabor, G. L.,

Abril, J. F., Agbyani, An, An, H. J., Andrews-Pfannkoch, C., Baldwin, D.,

Ballew, R. M., Basu, A., Berman, B. P., Bhandari, D., Bolshakov, S.,

Beeson, K. Y., Benos, P. V., Berman, B. P., Bhandari, D., Bolshakov, S.,

Chandra, I., Cherry, J. M., Cawley, S., Dahlke, C., Davenport, L. B.,

Dietz, S. M., Dodson, K., Doup, L. E., Downes, M., Dugan-Rocha, S.,

Dietz, S. M., Dodson, K., Doup, L. E., Downes, M., Dugan-Rocha, S.,

Gelbart, W. M., Glasser, K., Glodek, A., Gong, F., Gorrell, J. H., Gu, Z.,

Guan, P., Harris, M. L., Harris, N. L., Harvey, D., Heiman, T. J.,

Hernandez, J. R., Houck, J., Hostin, D., Houston, K. A., Howston, K. A.,
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Drosophila melanogaster chromosome 2L section 51 of 83 of the
                                                                                                                                                          803 GCAGCAGTAGCAGCAGCAACAGCAGCAACAACAGCAGCACGCAAATATTAAACGGACTTA
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                                                                                                                159760 ATCATATTTAACTAAATATATAGAAATTTAGAAAATAATTGCACCCTCAGCACTTGAATT
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Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.E., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., McIntosh, T.C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., May, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V. Park, S., Patel, S., Pfelifer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapheron, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Direct Submission

AL Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, Berkeley National Laboratory, MS 64-121

Lawrence submitted by:

Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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89.0%; Pred. No. 3.5e-201;
Live 0; Mismatches 13; Indels 98; C
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VCHONEYLDDETROFCRPKCSQSCGTHEECVAFGCDCSPGYRRTPDLGCQPVCAPDC
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                                                                                                 /locus_tag="CG31765"
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Svans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y.,
Banzon, J., An, H., Baldwin, D., Banzon, J., Besonn, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferrieras, S., Frise, E., Galle, R.F., Gargy, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D.,
Willams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M.
Sequencing of Drosophila melanogaster genome
Wel, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke2.,
Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,
Kravitz, S., Kulp, D., Laliz, L., Lasko, P., Lei, Y., Lerisky, A.A.,
Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C.,
McIntosh, T., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C.,
Moris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L.,
Muzny, D.M., Nelson, D.L., Nelson, K.A., Nixon, K.,
Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,
Pollard, J., Purl, V., Rese, M.G., Reinert, R., Remington, K.,
Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden Kiamos, I.,
Stapleton, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C.,
Stapleton, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C.,
Stapleton, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C.,
Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodager,
Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodager,
Worley, K.C., Wu, D., Yang, S., Yao, O.A., Yed, J., Yeh, R.F.,
Zaveri, J.S., Zhan, M., Zhou, X., Zhu, S., Zhu, X., Smith, H.O.,
The genome sequence of Drosophila melanogaster
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Submitted (23-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Sep 16, 2002 this sequence version replaced gi:7298121.
Location/Qualifiers
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Submitted (06-SRP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 27521)
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Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L.,
Misra, S., Crosby, M.A., Huang, Y., Kaninker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de
Grey, A.D.N.J., Harris, N.L., Kronmiller, B., Marshall, B.,
Millburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E.,
Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Rubin, G.M., Mungall, C.J. and Lewis, S.E.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="2L"
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UNCOMUNIOR DIAM LINEAR LIN 21 MAR'-ZUOU DIAMORIANIA DIAMORIANIA MEDIAGRASEA: CHROMOSOME ZL, region 34C4-36A7 (Adhrosophila melanogaster, chromosome ZL, region 34C4-36A7 (Adhrosophila melanogaster, chromosome ZL, region 34C4-36A7 (Adhrosophila melanogaster, chromosome ZL, region 34C4-36A7 (Adhrosophila MED001408 AC001629 L39638 L39638 L34362 L42040 L43450 AC001629 E139632 L39632 L39622 L39630 AC000578 L39635 L42041 L39637 L39632 L39631 L39635 L42072 L39763 L39763 L397751 L43449 L39626 L39620 L39632 AC00160 L39775 L42079 L39776 L43476 L39776 L43476 L39761 L49185 L42079 L39775 L42077 L42077 L39775 L42077 L39776 L39776 L43478 L42068 L49184 L39755 L42074 L42070 L39756 L42076 L39776 L43481 L43078 L42079 L46893 L46892 L46891 L43472 L42070 L39759 AC001602 AC001603 AC001303 AC000608 AC001303 AC000613 AC000613 AC000613 AC000613 AC000614 AC00614 AC00659 AC000650 AC000561 AC000561 AC000562 AC000386 AC000558 AC000556 AC000560 AC000561 AC000562 AC000561 AC000563 AC000565 AC000566 L39683 L39684 L43423 AC000566 L39683 AC000566 L39683 AC000565 AC000565 AC000386 AC000564 AC000565 AC000566 L39683 AC000565 AC000565 AC001301 AC000618 AC000565 AC000565 AC000386 AC000564 AC000565 AC000566 L39683 AC000566 L39681 L39434 AC0006625 AC001301 AC0006564 AC000565 AC000566 L39683 AC000566 L39683 AC000565 AC000566 L39683 AC000565 AC000566 L39683 AC0006625 AC001304 AC006625 AC000565 AC000565 AC000566 AC000566 L39683 AC0006625 AC001304 AC006625 AC000565 AC000566 AC0006625 AC001797 AC006625 AC001797 AC006625 AC001797 AC006625 AC001797 AC006626 AC001797 AC006626 AC000566 AC000628 AC001797 AC006626 AC000626 AC000626 AC000626 AC000626 AC000626 AC000626 AC000626 AC000626 AC000626 AC006626                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Rephydroidea; Drosophilae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

I (bases 1 to 320754)
Sabburner, M., Misra, S., Roote, J., Lewis, S.E., Blazej, R., Davis, T.,
Boyle, C., Galle, R., George, R., Harris; N., Hartzell, G., Harvey, D.,
Hong, L., Houston, K., Hoskins, R., Johnson, G., Martin, C.,
Man, K., Whitelaw, K., Celniker, S. and Rubin, G.M.
An exploration of the sequence of a 2.9-Mb region of the genome of
                                                                                                                                                                                                                                                                                        INV 21-MAR-2000
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Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Cieslolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,M., Moshrefi,M., Woshrefi,M., Woshrefi,M., Sir,E., Petelfer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
                                                                                                                                                                                       AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAGGATCGCAGCGAGCA
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                                                                                CCACGGCCACATTCGCCTGGGTGTTGCATGTGCTGCAGGTGCTGCTGCTGTCGCTGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBgn0028542"
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                                                                                                                                                                                                                   PLGCGNGVCDERNECKCREGYSLEPETRXYCQPECKFGCSFGRCVAPNKCACLDGYRL
AADGSCEPVCDSCENGKCTAPGHCNCNAGYLKLQGRCEPICSIPCKNGRCIGPDICEC
ASGFEWDRKSAECLPRCDLPCLNGVCVGNNQCDCKTGYVRDEHQRNICQPHCPQGCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565
                                                                                                                                                                                               MSRIQVCCDGYERNPHIYRRCEPICADDCRNGICTAPNTCVCIPGHVRTAEGKCISTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAGCAACATTGCAAGCGAGCACCACAATAGCCAGCAACAGGAGCCAGCATCGAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGCAACATGTTGTCGCCAAAGACAGCCGCAGCAGCAACTGCTGCCGGCGATGAAGCA
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13:14:17 PST 2002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 776.2; DB 3;
Pred. No. 3.7e-201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="CG33115-RA"
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89.0%;
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On or before Mar 22, 2000 this sequence version replaced 91:237897, gi:1945578, gi:2337896, gi:2337897, gi:1945578, gi:2337894, gi:3097819, gi:1995619, gi:3097823 gi:3097819, gi:1995619, gi:1007822 gi:1007822 gi:1007822 gi:1007822 gi:100782 gi:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="symbol-adat; synonym=BG:DS00941.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.fruitfly.org/publications/Adh.html
The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v
1.2.
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Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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                                                                                                                                                                                      Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:7227"
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1. .320754
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                                                      Rubin, G.M.
Direct Submission
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                                                                                                                  TITLE
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version: '(2.0a19MP-WashU [05-Feb-1998] [Build sol2.5-ultra 01:47:30 05-Feb-1998] , score: '121.0', scores: '121.0', scores: '121.0', organism: HOMO SAPIENS (HUMAN). dbxref: GenBank; AC004000; 92772565; -'', species: ''HOMO SAPIENS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DASGKKVVVTRHTKNMGKFSSVTVSTIDEEEDEIEAREIADSYANNARIIEKQLQRKG
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7603. .8493,8562. .9195,9261. .9751)
/note="symbol-5os"
/jone="Sos"
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PID:g158485.', species:'Drosophila melanogaster';
match-method:'BLASTX'', version:'2.0a19MP-WashU
[05-Feb-1998] [Bulld sol2.5-ultra 01:47:30 05-Feb-1998]'',
score:'889.0'', desc:''trEMBL::Q07888:SON OF SEVENLESS 1
PROTEIN (SOS 1). dbxref:GenBank; L13857; g306778: --'',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAFVYFDY IKHLKDLSSSQDDIESFEQVQGLLHPLHCDLEKVMASLSKERQVPVSGRV
WCOLAIERTRERELQMKVEHWEDKDVQONCNEFTREDSLSKLGSGKRIMSERKVFLEDGL
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01-APR-2003

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/traislation="MSEPOPHSLPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH
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VDRLCLIIFTLFTIIATLAVLFSAPHFIVSGVRG"
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                                                                                                                                     bp mRNA linear INV 01-APR-20 for nicotinic acetylcholine receptor
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases i to 1683)
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Dalpha7"
                                        melanogaster'
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Pred. No. 6.8e-130;
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Drosophila melanogaster mRNA for nicc
subunit Dalpha7 (nAcRalpha-18C gene)
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Submitted (31-MAR-2003) Millar N.
University College London, Gower

    1. .1683
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/mol_type="mRNA"

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KPRRONOTNSSSKLSNSTSSVAAAAASSTATSIATASAPSLHASSIMDAPTAAAANA
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VVSPRHEVMANNNSTLASASAMOVYFSPALPEHLPPQSLPDSNPFASDTEAPRAPKL
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LSPPPIPPRLNHSTGISYLRQSHGKSKEFVGNSSLLLPNTSSIMIRRNSAIEKRAAAT
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                                                                                                                Length 320754;
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                                                                                                                33.6%; Score 776.2; DB 3;
llarity 89.0%; Pred. No. 3.9e-201;
Conservative 0; Mismatches 13;
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1033 TTAATGCAAATTATCGATGTGGACGAAAAATCAATTGCTAGTCACTAATGTGTGGTTA 1092  1	1393 GATTTACAAGTTGTGAAATTGGTTGGTGGACCTACGATGGGTTTCAGTTG 598  1393 GATTTACAATTACAAGATGAAATTTGGTTCGTGGACCTACGGTTTCAGTTG 598  1393 GATTTACAATTACAAGATGAAACTGGCGGTGATACAGCTTACGTCGCCAACGGCGAG 1452	1633 CCAGATTCGGGTGAAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTT 1692	1762 TTGTGCTGGCTGCCATGGATATTGCGAATGAGTCGCCCAGGACGACCGCTGATCCTAGAG 1821
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HLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDH
LMQIIDVDEKNQLLITNIWLKLEWNDMLRWNTSDF
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SRPGSATTPPPARVPPPDFDLELRERSSKSLLANVLD
ERNGAGLAAHSCFGVDYELSLILKEIRVITDQMRKD
IIFTLFTIINTLAVLLSAPHIMVS*

1 others
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                                                                                                                           AGGAAATTCGCTTTATAACTGATCAGCTA 2163
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                                                      CGGTCACCCATCATACGTGCATCAAATCA
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era; Glossata; Ditrysia;
e; Heliothis.
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	S 4 S 5 S S S S S S S S S S S S S S S S	DAYER AG (DE)  Location/Qual;  Location/Qual;  Anol_type="ger" Ageref" ax 335. 1825  Anote="unnamed Codon_start=" Area" Ageref" ax 335. 1825  Anote="unnamed Codon_start=" Area" Ageref" ax 335. 1825  Anote="unnamed Codon_start=" Area" Ageref" area" Ageref" area" Ageref	N  ry Match  t Local Similarity 62.5%; Scort Scort Score 878; Conservative 0; M  925 GGATATCATGAAAAGAGACTGTTA
Query Match         22.2%;         Score 512.8;         DB 3;         Length 3629;           Best Local Similarity         62.5%;         Pred. No. 4.1e-129;         4;           Matches 878;         Conservative         0;         Mismatches 502;         Indels 24;         6aps 4;           Matches 878;         Conservative         0;         Mismatches 502;         Indels 24;         6aps 4;           Oy         925         GGGTACCACGAGAGCGGTACTGGTTTTTGGACCTTATAATACTTGGAGGG 84           Oy         985         CCCGTTCTCAATGAATCGACCACTACACTATGGTTTAATGCAATTTAATGCAATT         104           Oy         985         CCCGTTCTCAAGGAGCGCCCGTGGAGCTCTCTCGGCTTCACGCTTCAGGATC         54           Oy         1045         ATCGATGGACGAGAAAAATCAATTGCTACTACTAATAAACTTGGCTTAAAACTTGGATGAGT         54           Oy         1045         ATCGACGGAGAGAAAAACAACTGCTACTAATAACAAACTGGCTAAAACTGGATGGGATGGGATGGAGGGACGAAGAACACTTCAGATTTAATAACAAAACTGGCAGAAAACAACAACAACAACAACAAACA	1285 CCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAG 1344	1525 ATCACCTTGGCCATCATCCGCGAGGAACACTGTACTATTCTTCAACCTGATCAT 1584  1025 ATCACCTTGGCGTGGTGTGCGGGGGGAAACGGTTCTTCTTCAACTTGGTG 1084  1025 ATCACGTTGGGTGGTGTCGGGGGGGGGTCACTTCTTCAATTGGTG 1084  1585 CCTTGTGTACTGGTTGCCTCGGGGGTCACTGCTCGCGGTTGGTG 1084  1085 CCTGGGTGTTGCCTCGTGGCCTTGTGGGTTGCTCGCGGTTGCTCGGGT 1644  1085 CCTGGGTGTTGCTTGGTTTTGGGGTTCACTTGGGGTTCTCGAATTGGGT 1704  1145 GAAAAATTATGGCTGGGTGTTACCATGGTTCTGGACGGTTTCTGAATATGGTT 1704  1145 GAAAAATTATGGTGTTACATGTTGCTCTGGTGGTGTTCTCAACATGGT 1204  1705 GCGGAGACGATGGTGGGGGTGTTCCGTTGGCGTTGCTCCAACATGGT 1752  1111	cgccacgcacacactcacgaatgagtgattgattgattgcttgc

Qy         2047 CCAATTGGCAGCACCGGATGCGGTCACCCATCATACGTGCATCAAATCATCA         2106           b         1565 TACAGGGGGGTGAGAATGCCGGGGTTGGCGCACAGTTCTCGGT 1618           Qy         2107 ACTGAATATGGTTAAATGTTAAAGGAAATTCGCTTATAACTGATCAGCTACGT 2166           I	RESULT 13 E58347 LOCUGS E58347 LOCUGS E58347 LOCUGS DEFINITION Nucleic acid encoding insect actyl choline receptor subunit. ACCESSION E58347 ACCESSION E6847 ACCESSION E58347 ACCESSION E58347 ACCESSION E5847 ACCESSION E6847 ACCESSION E5847 ACCESSION E6847 ACCESSIO	PF 26-APR-1999 JP 1999118159	Querry Match         22.2%;         Score 512.8;         DB 6;         Length 3701;           Best Local Similarity         62.5%;         Pred. No. 4.1e-129;         Indels 24;         Gaps 4;           Matches 878;         Conservative         0;         Mismatches 502;         Indels 24;         Gaps 4;           Qy         925         GGATATCATGAAAGAGACTGTTACACGATCTTTTGGATCTTATAATACATTGAAGGT 984           Db.         425         GGGTACCAGAAAGAGGGTACTACAATTAGACCTATAATGAACTTTAATGAAGGTACTGAAGAGG 484           Qy         985         CCCGTTCTCAATGAATCAGACCGCTTACAATTAAGCTTTAATGAAATT         1044           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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AATGAAAATTTGCAGGTATGGTCGTTGAC 2226
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                                                                                                                                                                 bp DNA linear PAT 18-JUN-2001 actyl choline receptor subunit.
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doptera; Glossata; Ditrysia;
.hinae; Heliothis.
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No. 4.1e-129;
matches 502;
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PPFDDQHCEMKFGSWTYDGNOLDLVINSEDGGDLSDFITNGEWYLLAWFGKKNTIVYA
CCPEPYVDITFTIQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
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DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELOFITARWKRADD
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DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITW
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                                                                                                                                                                                                                                                                                                                AF321445 2023 bp mRNA linear INV 29-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type I (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
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                                                                                                               Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
Now and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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/gorde="lon channel; neurotransmitter transmembrane
/note="lon channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a and
                                 AAAGATGACGAGTGCAATGACATTGCCAATGATTGGAAATTTGCAGCTATGGTCGTTGAC
                                                                                            AGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCACAATAGCTGTACTA
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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1. .2023
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                                                                                                                                                                                                  /dev_stage="embryo"
1. .2023
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AF321445.1 GI:20152844
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                                          AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA
                                                           GACGGCACCTACCAGACGAACGTGGTGGTGCGGAACAACGGCTCGTGTCTATACGTTCCG
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                                                                                                                                  1971 GCCCGGCGGAACACTGCCACACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGA
   1449 CGAGTGGGAACTACTGGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCC
                            CGAGTGGTACTTGCTTGCCATGCCGGGAAAGAAGAATACGATAGTCTACGCCTGCTGCCC
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                                                                            CTTCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCT
                                                                                                                                                                                GCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGT
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                /note="results in serine deletion; compared to variant
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/note="results in asparagine to glycine substitution; compared to variant clone"
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Pred. No. 2.4e-111;
0; Mismatches 570; Indels
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/replace="t"
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/gene="nAcRalpha-30D"
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compared to variant clone"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  1 (bases 1 to 2023) Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphae and Dalpha, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002) 2 (bases 1 to 2023) 2 (bases 1 to 2023) Grauso,M. and Sattelle,D.B. Direct Submission Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OXI			/protein_id="AAM13394.1" /db_xref="di:20152849" /db_xref="di:20152849" /translation="MDSPLPASLSLEVLIFIAIIKESCOGPHEKRLLNHLLSTVNTL ERPVANESEPLEVKEGLTLQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVK DERTPWKMKPDVLAWYNSADGEFOGTYHTNLYWFHSGSCLYVPPGTEKSTCKMDITW FPEDDQHCDWKFGSWTYDGNGLDLVLNSEDGEDLSDFTNGEWYLLAMPGKRWTIVYA CCPEDYVDITFTIQIRRRTLYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL ESTIVFLANVAETLEQYSDAIPLGTYFNCITHEWASSVVLTVVVLNYHHRTADIHEM PWIKSVFLQMLPWILLRMGRPGKRITRRTILLSNRMKELELKERSSKSLLANVLDIDD DFRHTISGSGTAIGSSASFGRETTVEEHHTAIGCNHKDLHLILKELQFTTARMRKADD EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ" //ADYG="DAGP210ha-30p" //ADYG="DAGP210ha-30p"	/gene="results in glycine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" /replace="a" /agene="nAcRalpha-30D" /note="results in asparagine to serine substitution; /compared to the sequence deposited in GenBank Accession //order="results in asparagine"/	546 a tch al Similari 824; Cons 909 TAAAGTT	441 TAAAGAAAGCTCCAAGGACCTCATGAAAGCGCCTGCAGAACTGCTGTCCCACTA 500 969 TAATACACTACGACGCTCCAATGAATGGACCGCTACAATAAGCTTTGGTT 1028 969 TAATACACTAGGACGCCCAATGAATGGATCGGAGCCCTTACAATAAGCTTTGGTT 1028 969 TAATACCCTGGAGCGCCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACT 560 1029 AACTTTAATGCAAATTATCGATGGAGAAAAATCAATTGCTAGTCTAATGTGTG 1088
REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUT CE	gene	vari	vari	BASE COUNT ORIGIN Query Match Best Local Matches 82	oy Oy Oy

1700	2210	1760	2270	1820
1641 CACGGCCATCGGCTGCAATCACAAAGATCTTCATCTAATTCTCAAAGAATTGCAATTAT 1700	2151 AACTGATCAGCTACGTAAAGATGACGAGTGCAATGACATTGCCAATGGATTGGAATTTGC 2210	1701 TACGGCGCGGGATGCGCAAAGCTGACGACGGAATTGATGGCGGATTGGAAGTTCG 1760	2211 AGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCAC 2270	1761 GGCAATGGTTGTGTTTTGTTTTTTTTTCACGCTCTTCACGATATTGTTTTCACGCTCTTCACGATATTGTATTCACGAATATTGTTTTCACGCTCTTCACGATATTGTATTGTTTTCACGCTCTTCACGATATTGTATTGTTTTCACGCTCTTCACGATATTGTATTGTTTTCACGCTCTTCACGATATTGTATTGTTTTCACGCTCTTCACGATATTGTATTGTATTGTTTTCACGCTCTTCACGATATTGTATT
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